

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 212.175 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAMWLLILIMVHPGSCALW.....GTHCHSSDGRGVPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	916	89.8	180	1 NCT3_MACMU	Q8MJ02 macaca mula
2	896	87.8	176	1 NCT3_MACFA	P61483 macaca fasc
3	876	85.9	201	1 NCT3_HUMAN	O14931 homo sapien
4	868	85.1	201	1 NCT3_PANTR	P61484 pan troglod
5	606	59.4	192	1 NCT3_RAT	Q8C89 rat mus norv
6	136.5	13.4	235	2 Q99M11	Q99M11 mus musculu
7	123.5	12.1	313	2 Q6IPU1	Q6IPU1 homo sapien
8	123.5	12.1	313	2 AAH71724	AAH71724 homo sapi
9	120.5	11.8	234	2 Q6GMW3	Q6GMW3 homo sapien
10	119.5	11.7	221	2 Q28090	Q28090 bos taurus
11	117.5	11.5	221	2 Q7631	Q7631 ovis aries
12	115.5	11.3	223	2 Q62859	Q62859 rattus norv
13	114.5	11.2	223	2 Q7TMX1	Q7TMX1 mus musculu
14	112.5	11.0	223	2 Q7JHU0	Q7JHU0 macaca neme
15	112.5	11.0	223	2 Q7JHU2	Q7JHU2 cercocobus
16	112.5	11.0	223	2 Q9BDC4	Q9BDC4 macaca mula
17	112.5	11.0	223	2 Q9BDN7	Q9BDN7 papio anubi
18	112	11.0	223	1 CTL4_HUMAN	P64410 homo sapien
19	112	11.0	223	2 AAC17066	AAC17066 homo sapi
20	112	11.0	223	2 AAH70162	AAH70162 homo sapi
21	112	11.0	223	2 AAH69566	AAH69566 homo sapi
22	112	11.0	700	2 Q7TSU7	Q7TSU7 mus musculu
23	112	11.0	700	2 BAC33658	BAC33658 m es cell
24	111.5	10.9	226	1 C79A_HUMAN	P11912 homo sapien
25	110.5	10.8	223	2 AAH42741	AAH42741 mus muscu
26	110.5	10.8	234	2 Q6GMV8	Q6GMV8 homo sapien
27	110	10.8	233	2 Q96169	Q96169 homo sapien
28	110	10.8	237	2 Q6DHW4	Q6DHW4 homo sapien
29	109.5	10.7	240	2 Q6MG96	Q6MG96 rattus norv
30	109.5	10.7	240	2 CAE83950	CAE83950 rattus no
31	109	10.7	172	2 Q7LAW3	Q7LAW3 bos taurus

## ALIGNMENTS

### RESULT 1

ID	NCT3_MACMU	STANDARD;	PRT;	180 AA.
AC	Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).			
GN	Name=NCR3;			
OS	Macaca mulatta (Rhesus macaque).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;			
OC	Cercopitheciinae; Macaca.			
OX	NBI_TaxID=9544;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.			
RA	LaBonte M.L., Miller J., Letvin N.L.;			
RT	"Molecular cloning of rhesus monkey NKP46 and NKP30 and identification of NKP46SD and NKP30S."			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.			
RC	TISSUE=Lymphoid;			
RA	Rizzi M., Biassoni R.;			
RL	"NCR express by macaca NK cells."			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).			
CC	-!- SUBUNIT: Interacts with CD32 (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=4;			
CC	Name=1;			
CC	IsoId=Q8MJ02-1; Sequence=Displayed;			
CC	Note=No experimental confirmation available;			
CC	Name=2;			
CC	IsoId=Q8MJ02-2; Sequence=VSP 010414;			
CC	Note=No experimental confirmation available;			
CC	Name=3;			
CC	IsoId=Q8MJ02-3; Sequence=VSP 010415, VSP 010416;			
CC	Note=No experimental confirmation available;			
CC	Name=4;			
CC	IsoId=Q8MJ02-4; Sequence=VSP 010417;			
CC	Note=No experimental confirmation available;			
CC	-!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.			
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like domain.			
CC	-----			
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DR EMBL; AY035214; AAK63116.1; -  
 DR EMBL; AY035215; AAK63117.1; -  
 DR EMBL; AY035216; AAK63118.1; -  
 DR EMBL; AY035217; AAK63119.1; -  
 DR EMBL; AY035218; AAK63120.1; -  
 DR HSSP; PJ6410; 1185.  
 DR InterPro; IPR003599; IG  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS00835; IG-Like; 1.  
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain;  
 KW Polymorphism; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 18  
 FT CHAIN 19 180  
 FT Natural cytotoxicity triggering receptor  
 FT 3.  
 FT DOMAIN 19 133  
 FT TRANSMEM 134 154  
 FT DOMAIN 155 180  
 FT DOMAIN 181 196  
 FT DISULFID 39 108  
 FT CARBOHYD 42 42  
 FT CARBOHYD 121 121  
 FT VARSPLIC 66 90  
 FT VARSPLIC 112 115  
 FT VARSPLIC 116 180  
 FT VARSPLIC 177 180  
 FT VARSPLIC 156 156  
 FT VARIANT 156 156  
 FT SEQUENCE 180 AA; 19639 MW; 5C2DF53487B2A3B6 CRC64;

Query Match 89.8%; Score 916; DB 1; Length 180;  
 Best Local Similarity 95.0%; Pred. No. 2.1e-74;  
 Matches 171; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MAMLLILIMVHPGSCALWVSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60  
 DB 1 MAMLLILIMVHPGSCALWVSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHVDVRGHDASIVYCRVEVLGLGVGTG 120  
 DB 61 APGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHVDVRGHDAGIYVCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHGTHCHSDGP 180  
 DB 121 NGTRLVVEKEYPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHGTHCHSDGP 180

RESULT 2  
 NCT3 MACFA STANDARD; PRT; 176 AA.  
 ID NCT3 MACFA  
 AC P61483; Q95JB8;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
 GN Name=NCR3;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OC NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RA Rizzi M., Blassoni R.;

RT "Non MHC specific natural cytotoxicity receptors (NCR) expressed in  
 RT Macaca fascicularis lymphoid cells."  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
 CC the increased efficiency of activated natural killer (NK) cells to  
 CC mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
 CC -----

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DR EMBL; AJ278389; CAC41081.1; -  
 DR HSSP; PJ6410; 1185.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-Like.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS00835; IG-Like; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 18  
 FT CHAIN 19 176  
 FT DOMAIN 19 135  
 FT TRANSMEM 136 156  
 FT DOMAIN 157 176  
 FT DOMAIN 19 126  
 FT DISULFID 39 108  
 FT CARBOHYD 42 42  
 FT CARBOHYD 121 121  
 FT SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;

Query Match 87.8%; Score 896; DB 1; Length 176;  
 Best Local Similarity 95.5%; Pred. No. 1.3e-72;  
 Matches 168; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAMLLILIMVHPGSCALWVSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60  
 DB 1 MAMLLILIMVHPGSCALWVSQPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHVDVRGHDASIVYCRVEVLGLGVGTG 120  
 DB 61 APGKEVRNGTPEFRGLAPLASSRFLDHQAEHLHVDVRGHDAGIYVCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHGTHCHS 176  
 DB 121 NGTRLVVEKEYPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHGTHCHS 176

RESULT 3  
 NCT3 HUMAN STANDARD; PRT; 201 AA.  
 ID NCT3 HUMAN  
 AC O14931; O14930; O14932; O95667; O95668; O95669;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
 GN Name=NCR3; Synonyms=1C7;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH  
 RP CD32, AND FUNCTION.



FT AKSTLGGPQL (in isoform 3 and isoform 6).  
 FT /FTID=VSP\_010412.  
 FT LTMGPRRLPVPAPLPVPPGSAHLPPVPG -> HC  
 FT HMGTHCHSSDGRGVPEPRCP (in isoform 2 and  
 FT isoform 5)  
 FT /FTID=VSP\_010413.  
 FT /FTID=VSP\_010413.  
 SQ SEQUENCE 201 AA; 21593 MW; 2855AB46902D429 CRC64;

Query Match 85.9%; Score 876; DB 1; Length 201;  
 Best Local Similarity 89.2%; Pred. No. 9.4e-71;  
 Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPEIRTLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 DB 1 MAWMLLLILIMVHPGSCALWVSQPPPEIRTLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVWEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 DB 121 NGTRLVWEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 QY 181 R----GVPEPRCP 190  
 DB 173 RRLPVPVAPLPP 186

RESULT 4  
 NCT3 PANTR STANDARD; PRT; 201 AA.  
 ID NCT3 PANTR STANDARD; PRT; 201 AA.  
 AC P61484;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (Nkp30) (NK-p30).  
 GN Name=NCR3;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymphoid;  
 RA Biassoni R.  
 RL "Characterization of natural killer receptors in chimpanzees."  
 Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
 CC the increased efficiency of activated natural killer (NK) cells to  
 CC mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD3Z (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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 CC -----  
 CC EMBL; AJ516006; CAD56759.1;  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 201 Potential.  
 FT CHAIN 19 181 Natural cytotoxicity triggering receptor  
 FT 3.  
 FT DOMAIN 19 135 Extracellular (Potential).  
 FT TRANSMEM 136 156 Potential.

FT DOMAIN 157 201 Cytoplasmic (Potential).  
 FT DOMAIN 19 126 Ig-like.  
 FT DISULFID 39 108 By similarity.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 201 AA; 21656 MW; 3768ACC768BD749 CRC64;

Query Match 85.1%; Score 868; DB 1; Length 201;  
 Best Local Similarity 88.7%; Pred. No. 4.9e-70;  
 Matches 172; Conservative 2; Mismatches 8; Indels 12; Gaps 2;

QY 1 MAWMLLLILIMVHPGSCALWVSQPPPEIRTLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 DB 1 MAWMLLLILIMVHPGSCALWVSQPPPEIRTLGGSAFLPCSFNASQGLAIGSVTWFRDEV 60  
 QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIIYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVWEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 DB 121 NGTRLVWEKEHPQLGAGTVLLLRAGFYAVSFLSVAGSTVYQKCHCHMGTHCHSDGP 180  
 QY 181 R----GVPEPRCP 190  
 DB 173 RRLPVPVAPLPP 186

RESULT 5  
 NCT3 RAT STANDARD; PRT; 192 AA.  
 ID NCT3 RAT STANDARD; PRT; 192 AA.  
 AC Q8CFD9; Q80WM8; Q8CG11;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (Nkp30) (NK-p30).  
 GN Name=Ncr3; Synonyms=1C7;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-7; VAL-19; VAL-82 AND THR-138.  
 RC STRAIN=PVG; TISSUE=Natural killer cells.  
 RX PubMed=12548565; DOI=10.1002/immu.200310008;  
 RA Backman-Petersson E., Miller J.R., Hollyoake M., Aguado B.,  
 RA Butcher G.W.;  
 RT "Molecular characterization of the novel rat NK receptor 1C7".  
 RL Eur. J. Immunol. 33:342-351(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Lewis;  
 RX MEDLINE=22168131; PubMed=12180816;  
 RA Hsieh C.L., Obara H., Ogura Y., Martinez O.M., Krams S.M.;  
 RT "NK cells and transplantation".  
 RL Transpl. Immunol. 9:111-114(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Brown Norway;  
 RX PubMed=15057822; DOI=10.1038/nature02426;  
 RA Gibbs R.A., Weinstein G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,  
 RA Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,  
 RA Hites S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,  
 RA Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,  
 RA Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferreira S.,  
 RA Fiesler C., Glodok A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,  
 RA Frannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,  
 RA Smith D., Lee H.M., Gustafson E., Cahill P., Kana A.,  
 RA Doucette-Stamm L., Weinstein K., Fichtel K., Weiss R.B., Dunn D.M.,  
 RA Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,  
 RA Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,  
 RA Krzyzanski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,



RA Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,  
RA Abramson S., Nierman W.C., Havlik P.H., Chen R., Durbin K.J., Egan A.,  
RA Ren Y., Song X.Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,  
RA D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,  
RA Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,  
RA Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzov E.,  
RA Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E.,  
RA Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,  
RA Young J.M., Huang H., Wang H., King H., Daniels S., Gietzen D.,  
RA Schmid J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,  
RA Arlil J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,  
RA Poliakov A., Hubner N., Ganten D., Goesele C., Hummel O., Kretzler T.,  
RA Lee Y.A., Monti J., Schulz H., Zimdahl H., Himmelbauer H., Lehrach H.,  
RA Jacob H.J., Bromberg S., Gullings-Handley J., Jensen-Seaman M.I.,  
RA Kiteck A.E., Lazar J., Pasko D., Tonelliato P.J., Twigger S.,  
RA Ponting C.P., Duarte J.M., Rice S., Goodstadt L., Beatson S.A.,  
RA Eses R.D., Winter E.E., Webber C., Brandt P., Nyakatura G.,  
RA Adetobi M., Chiaronello F., Elntski L., Eswara P., Hardison R.C.,  
RA Hou M., Kolbe D., Makova K., Miller W., Nekrutenko A., Riener C.,  
RA Schwartz S., Taylor J., Yang S., Zhang Y., Lindpaintner K.,  
RA Andrews T.D., Caccamo M., Clamp M., Clarke L., Curwen V., Durbin R.,  
RA Eyas E., Searle S.M., Cooper G.M., Batzoglou S., Brudno M., Sidow A.,  
RA Stone E.A., Payseur B.A., Bourque G., Lopez-Otin C., Puente X.S.,  
RA Chakrabarti K., Chatterji S., Dewey C., Pachter L., Bray N., Yap V.B.,  
RA Caspi A., Tesler G., Pevzner P.A., Hausler D., Roskin K.M.,  
RA Baertsch R., Clawson H., Furey T.S., Hinrichs A.S., Karolchik D.,  
RA Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N.,  
RA Stenson P.D., Ma B., Brent M., Arumugam M., Shreynberg D.,  
RA Copley R.R., Taylor M.S., Riechman K., Mudunuri U., Peterson J.,  
RA Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F.,  
RA "Genome sequence of the Brown Norway rat yields insights into  
RT mammalian evolution.";  
RL Nature 428:493-521(2004).  
RN [4]  
RN IDENTIFICATION.  
RX PubMed:15060004; DOI=10.1101/gr.1987704;  
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,  
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.;  
RT "The genomic sequence and comparative analysis of the rat major  
RT histocompatibility complex.";  
RL Genome Res. 14:631-639(2004).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD3Z (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
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CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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CC -----  
DR EMBL; AJ430418; CAD32066.1; -  
DR EMBL; AJ430419; CAD32067.2; -  
DR EMBL; AJ430420; CAD32067.2; JOINED.  
DR EMBL; AY273824; AAP13457.1; -  
DR EMBL; BX883046; CAE84000.1; -  
DR HSSP; P09793; 1DOT.  
DR RGD; 727881; 1C7.  
DR InterPro; IPR003599; IG.  
DR InterPro; IPR007110; IG-like.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00409; IG; 1.  
DR PROSITE; PS00835; IG LIKE; 1.  
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;  
KW Transmembrane.  
FT SIGNAL 1 18 Potential.  
FT CHAIN 19 192 Natural cytotoxicity triggering receptor

FT DOMAIN 19 147  
FT TRANSMEM 148 168  
FT DOMAIN 169 192  
FT DOMAIN 19 126  
FT DISULFID 39 108  
FT VARIANT 7 7  
FT VARIANT 19 19  
FT VARIANT 82 82  
FT VARIANT 138 138  
FT CONFLICT 135 135  
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D2377 CRC64;  
Query Match 59.4%; Score 606; DB 1; Length 192;  
Best Local Similarity 64.8%; Fred. NO. 1.8e-46;  
Matches 116; Conservative 25; Mismatches 30; Indels 8; Gaps 1;  
QY 1 MAMMLLIIMVPGSCALWVSQPEIRTLGSSAFPCSFNASQGLAIGSVTFWRDEV 60  
DB 1 MAKVLLIVFIMVYAGSCALWVSQPEIRAQGGTASLPSCFNASRGKAAIGSATWYQDKV 60  
QY 61 VPGKEVRNGTPEFRORLAPLASSRFLHPOHLEHIDVRGHDASIVYCRVEVLGVGTG 120  
DB 61 AFGMELSNVTPGFRGRVASFSASQFIRGHKAGLLIQDIQSHDARIYVCRVEVLGVGTG 120  
QY 121 NGTRLVWEKEHPQ-----LGAGTVLLLRAGFYAVSFLSVAGSTVYVYQKCHCHMG 171  
DB 121 NGTRLVWEKEPQQASNAPEEAAYTSLLRAGVYALSVATSGSVYVYQKCLCHVG 179  
RESULT 6  
Q99M11 PRELIMINARY; PRT; 235 AA.  
ID Q99M11  
AC Q99M11; 01-JUN-2001 (TREMELrel. 17, Created)  
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_taxid=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Czech II;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schumetz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska J., Smalls D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=Czech II;  
RC TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC002129; AAH02129.1; -.
DR HSP; P01843; 1JUN.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS0290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match      13.4%; Score 136.5; DB 2; Length 235;
Best Local Similarity 31.2%; Pred. No. 0.0004;
Matches 43; Conservative 25; Mismatches 49; Indels 21; Gaps 7;

QY 1 MAMWLLILLIMVH-PGSCA-LVWVOPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRD 58
DQ 1 MWAPELLLVFHLHGTGSCAQLVLPQSVSTSLGSLAKLPC--KASTGNIGDSYVWYQQ 58
QY 59 -----EVVPGKEVRNG--TPEFRGLAPLASSRFLHQAELHIRDVRGHDAIYVCR 109
DQ 59 YNGRSPTNVIYGDLPSPGVSDRFGSDSSNSAF-----LTIQVQADDEADYQC 111
QY 110 VEVLGLGVGTNGTGLVV 127
DQ 112 SYSGSIRV-FGGGTRLV 128

RESULT 7
Q6IPU1 PRELIMINARY; PRT; 313 AA.
AC Q6IPU1.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071724; AAH71724.1; -.

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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 313 AA; 34612 MW; BF990C926CE361BC CRC64;

Query Match      12.1%; Score 123.5; DB 2; Length 313;
Best Local Similarity 25.7%; Pred. No. 0.008;
Matches 46; Conservative 26; Mismatches 62; Indels 45; Gaps 8;

QY 1 MAMWLLILLIMVH-PGSCA-LVWVOPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRD 58
DQ 6 LCWALLCLL---GAGSVETGVTSPTLIKT-RGQVTLRCSSQSGH-----NTVSWYQQ 56
QY 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHQAELHIRDVRGHDAIYVCRV 110
DQ 57 ALGQGPQIFQYREENG-----RGFPFRSGLOFPNYSSELNVNVALELDSALYLCA 112
QY 111 EVLGLGVGT-----NGTGLVV-----EKEHPQLGAGTVLLLRAGFY 147
DQ 113 SLGGPGLGETQVFGPTGLLVLELKNVFPPEVAFPESEAEISHTQATLVCLATG 171

RESULT 8
AAH71724 PRELIMINARY; PRT; 313 AA.
AC AAH71724.
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071724; AAH71724.1; -.
KW Hypothetical protein.

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[illegible]

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RESULT 10
Q28090 PRELIMINARY; PRT; 221 AA.
ID Q28090
AC Q28090;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CTLA-4 protein precursor.
DE Name=CTLA-4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=96186531; PubMed=9606060;
RX Parsons K.R., Young J.R., Collins R.A., Howard C.J.;
RA "Cattle CTLA-4, cattle CD28 and chicken CD28 bind human CD86 (B70),
RT although the MYPPPY hexapeptide is not conserved in cattle CD28.";
RL Immunogenetics 43:388-391(1996).
DR EMBL; X91305; CAA63708.1; -
DR HSP; P16410; I185
DR GO; GO:0015020; C:membrane; IEA.
DR GO; GO:0008955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG.1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG.1
DR PROSITE; PS00835; IG_LIKE; 1.
DR SIGNAL
FT SIGNAL
SQ SEQUENCE 221 AA; 24433 MW; 2CAF148422C597AA CRC64;
Query Match 11.7%; Score 119.5; DB 2; Length 221;
Best Local Similarity 28.6%; Pred. No. 0.013;
Matches 46; Conservative 24; Mismatches 80; Indels 11; Gaps 74
QY 6 LLILIMVPGSCALWVSOPPEIRILEGSAFLPCSFNASCGRLAISGVTWFRDEVVPGKE 65
DB 23 LFLFLVPIPVFSKGMNVTPPPVVLASSRGVASFSCYEES--GKADEVRTVTLREAGSQVTE 81
QY 66 VRNGTPEFRGRPLAPLASSRFEL--HDHQAELHIRDVGHGDAISYVCRVEVL---GLGVGT 119
DB 82 VCAGTVWEDELFTFDDSTCTGTSEGNKVNLTIGLRAMDTGLYCKVELMYPPPYVGI 141
QY 120 NGNTRLVWEKHPQLGAGTVLLLRA-----GPHYVSFLSVAV 156
DB 142 NGGTOYVDPBPSPDPSDFLWILAAVSSGFFFYSLITAV 182

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RESULT 11
O97631 PRELIMINARY; PRT; 221 AA.
AC Q97631;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytotoxic T-lymphocyte-associated protein 4.
GN Name=CTLA-4;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9309828; PubMed=10380709;
RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;
RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";
RL Immunogenetics 49:583-584(1999).
DR EMBL; AF092740; AAD04380.1; -.
DR HSSP; P16410; 1185.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG-like.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 221 AA; 24490 MW; D317B9D5557BA6FB CRC64;

Query Match 11.5%; Score 117.5; DB 2; Length 221;
Best Local Similarity 28.0%; Pred. No. 0.019;
Matches 45; Conservative 25; Mismatches 80; Indels 11; Gaps 4;

QY 6 LLLILMVHPGSCALWVSPPEIRTLGSSAFPLCP-----SFNASQRLAIGSVTFWFRDEV 65
DB 23 LFFLLFIPVSKGMVTPPVVLASSRGVASFCEYESS-GKADVVRVTLRKAGIQVTE 81
QY 66 VRNGTPEFRGRPLAPLASSRFL---HDHQAEHLHIRDVRGHDSIYVCRVEVL---GLGVGT 119
DB 82 VCACTYVVEDELTLDDSSCGISRGKNVNLTIQGLRDMDTGLYVCKVELMYPFYMGE 141
QY 120 GNGTRLVVEKHPOLGAGTVLLRA-----GFYAVSFLSVAV 156
DB 142 GNGRQIYVIDPEPCDSDFLWLAAVSSGLFFYSFLITAV 182

RESULT 12
O62859 PRELIMINARY; PRT; 223 AA.
AC Q62859;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytotoxic T-lymphocyte associated protein-4 precursor.
GN Name=CTLA-4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96134012; PubMed=8550107;
RA Oaks M.K., Penwell R.T., Tector A.J.;
RT "Nucleotide sequence of the ACI rat CTLA-4 molecule.";
RL Immunogenetics 43:173-174(1996).
DR EMBL; U37121; AAC52502.1; -.
DR HSSP; P09793; 1DQT.
DR GO; GO:0016020; C:membrane; IEA.

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DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG-like.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Signal.
FT SIGNAL 1 37 Potential.
FT CHAIN 38 223 Potential.
SQ SEQUENCE 223 AA; 24858 MW; C19EE4F242C6A87B CRC64;

Query Match 11.3%; Score 115.5; DB 2; Length 223;
Best Local Similarity 28.7%; Pred. No. 0.03;
Matches 48; Conservative 26; Mismatches 72; Indels 21; Gaps 7;

QY 5 LLLILMVHPGSCALWVSPPEIRTLGSSAFPLCP-----SFNASQRLAIGSVTFWFRDEV 60
DB 24 VLLSLFLPIFSEAIQTQPSVVLASSHGVSFPCPEYASSHTDEVRVTVLRQT--NDQV 81
QY 61 VPGKEVRNGTPEFRGLA----PLASSRFLHDHQAEHLHIRDVRGHDSIYVCRVEVL--- 113
DB 82 T---EVCATTFVTQNTLGLDDPFCSGTF--NESRVNLTIQGLRAADTGLYFCRVELMYP 137
QY 114 GLGVGTGNGTRLVVEKHPOLGAGTVLLRA-----GFYAVSFLSVAV 156
DB 138 PVFVGMGNGTQIYVIDPEPCDSDFLWLAAVSSGLFFYSFLITAV 184

RESULT 13
Q7TMX1 PRELIMINARY; PRT; 223 AA.
AC Q7TMX1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
DE Cytotoxic T-lymphocyte-associated protein 4.
GN Name=CTLA4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay D.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052683; AAH52683.1; -.

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DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG-like; 1.
SQ SEQUENCE 223 AA; 25035 MW; BE8E4C77E6A04549 CRC64;

Query Match 11.2%; Score 114.5; DB 2; Length 223;
Best Local Similarity 27.5%; Pred. No. 0.037;
Matches 46; Conservative 25; Mismatches 79; Indels 17; Gaps 6;

QY 3 WMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFRDVP 58
D 22 FVALLTLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPGKATEVRVTVLRQADSQ 80
QY 59 --EWPCKEVRNTPPEGRGLAPLASSRFLHDHQAELHTRDVRGHDAIYVCRVEVL--- 113
D 81 MTEVCATTFTEKNTVGFLD--YFPCSGTF-NESRVNLTIOGLRAVDTGLYCKVELMYP 137
QY 114 GLGVGTGNGTRLVVEKEHPQLGAGTVL-----LLRAGFYAVSFLSVAV 156
D 138 PYFVGNGNGRIYVIDPEPCDSDFLWLILVAVSLGLFFYSFLVTAV 184

RESULT 14
Q7JHJ0 PRELIMINARY; PRT; 223 AA.
ID Q7JHJ0
AC Q7JHJ0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CD152 protein precursor.
GN Name=CTLA-4;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecidae;
OC NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344848; AAK37608.1; -.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG V.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 223 AA; 24683 MW; BDE42248A00398FA CRC64;

Query Match 11.0%; Score 112.5; DB 2; Length 223;
Best Local Similarity 27.6%; Pred. No. 0.055;
Matches 47; Conservative 23; Mismatches 77; Indels 23; Gaps 5;

QY 3 WMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPLPCSFNASQGRLAIGSVTWFRDVP 62
D 22 YTLFLSLLFIPVFSKAMHVAQPAVVLANSRGIAFVCEY-ASPGKATEVRVTVLRQADSQ 80
QY 63 GKEVRNGTPEFGRGLAPLASSRFLHD-----HQAELHTRDVRGHDAIYVCRVEVL 113
D 81 VTEVCAATYMGNELT-----FLDSDICTGSSGNQVNLTIQGLRAMDTGLYCKVELM 134
QY 114 ---GLGVGTGNGTRLVVEKEHPQLGAGTVLLRA-----GFYAVSFLSVAV 156
D 135 YPPPYMGIGNGTQIYVIDPEPCDSDFLWLILAAVSSGLFFYSFLVTAV 184

Search completed: November 16, 2004, 19:14:29
Job time : 215.375 secs
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 39.3103 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-2  
Perfect score: 1020  
Sequence: 1 YANMLLLILIMVHPGSCALW.....GTHCHSDGPRGVIPEPRCP 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : FIR\_79.\*

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118	11.6	136	2 B45893	T-cell receptor al
2	117.5	11.5	132	2 A24402	T-cell receptor al
3	116	11.4	146	2 S26408	T-cell receptor be
4	115.5	11.3	232	2 S25756	Ig lambda chain -
5	111.5	10.9	226	2 A46477	membrane-bound imm
6	111	10.9	233	2 S25747	Ig lambda chain -
7	110	10.8	223	2 T09536	cytotoxic T-lympho
8	108.5	10.6	223	2 A29063	Ig lambda chain -
9	108	10.6	235	2 S25749	Ig lambda chain -
10	107.5	10.5	138	2 C27577	T-cell receptor al
11	106.5	10.4	131	2 D24032	T-cell receptor al
12	106.5	10.4	131	2 E24032	T-cell receptor al
13	106	10.4	132	1 RWMSCV	T-cell receptor al
14	104.5	10.3	131	2 F45893	Ig lambda chain v
15	104.5	10.2	132	2 S09713	CTLA-4 precursor -
16	103.5	10.1	223	2 I46696	T-cell receptor al
17	103	10.1	129	2 A42692	T-cell receptor al
18	102.5	10.0	110	2 B24032	T-cell receptor al
19	101.5	10.0	139	2 S36355	T-cell receptor de
20	101	9.9	120	2 I54487	T-cell receptor al
21	101	9.9	235	2 S14675	Ig lambda chain -
22	100.5	9.9	1694	2 S50065	sialoadhesin - mou
23	100	9.8	110	2 A24032	T-cell receptor al
24	99.5	9.8	271	2 A53268	T-cell receptor al
25	99	9.7	130	2 A31211	T-cell receptor al
26	98.5	9.7	128	2 S24319	Ig lambda chain pr
27	98.5	9.7	152	2 S21826	T-cell receptor be
28	98.5	9.7	236	2 S25746	Ig lambda chain -
29	98.5	9.7	247	2 A55717	myelin/oligodendro

30	98.5	9.7	526	2 S70587	butyrophilin presu
31	96	9.4	131	1 L6HUEB	Ig lambda chain pr
32	96	9.4	131	2 D24402	T-cell receptor al
33	95.5	9.4	140	2 PH0134	Ig lambda chain pr
34	95.5	9.4	218	2 B47112	myelin/oligodendro
35	94.5	9.3	108	2 JH0342	T-cell receptor al
36	94.5	9.3	186	2 S08614	cytotoxic T-lympho
37	93.5	9.2	247	2 S58394	myelin/oligodendro
38	93	9.1	117	2 I68824	T-cell receptor al
39	93	9.1	132	2 D45893	T-cell receptor al
40	93	9.1	246	1 A32999	myelin P0 protein
41	93	9.1	267	1 RWMSC8	T-cell receptor al
42	92.5	9.1	136	2 S42610	ARMVlambda protein
43	92.5	9.1	139	2 S36302	T-cell receptor de
44	92.5	9.1	403	2 I32590	m33-B isoform - mo
45	92	9.0	129	2 A30554	Ig lambda chain pr

ALIGNMENTS

RESULT 1

B45893  
T-cell receptor alpha chain precursor V region (BTA29) - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C;Accession: B45893  
R;Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A;Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A;Reference number: A45893; MUID:90129157; PMID:2137108  
A;Accession: B45893  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-136 <LSH>  
A;Cross-references: GB:D90011; NID:g217610; PIDN:BAAL4061.1; PID:g217611  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 11.6%; Score 118; DB 2; Length 136;  
Best Local Similarity 27.9%; Pred. No. 0.0017;  
Matches 41; Conservative 22; Mismatches 42; Indels 42; Gaps 9;

QY	4	MILLILIMV-----HPGSCALWVSPPEIRTLGGSAFLPCSPNAGRLAIGSVTWTF	56
DB	8	LLVILLASVDLRQPAEHSG-----AEPASLPVPEGAASLGCTYSDNSLY----	57
QY	57	RDEVVPGKEVRNGTPEF-----RGLAPLASSRFLHDHQAELHIRDVRGHDASI	105
DB	59	RQ--YFGK-----GPEFLQVYANNKKEGKT--AQSNKINKH-VSLIRDSEPSDSAT	107
QY	106	YVCRVVEVLGLVGT----GNGTRLVVE	128
DB	108	YLCAVDTTSTAGTKLTFTGEGTRLIVK	134

RESULT 2

A24402  
T-cell receptor alpha chain precursor V region (C5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997  
C;Accession: A24402  
R;Becker, D.N.; Patten, P.; Chien, Y.; Yokota, T.; Bshhar, Z.; Giedlin, M.; Gascoigne, T.  
Nature 317, 430-434, 1985  
A;Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.  
A;Reference number: A93368; MUID:86014379; PMID:2995827  
A;Accession: A24402  
A;Molecule type: mRNA  
A;Residues: 1-132 <BEC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor

Query Match 11.5%; Score 117.5; DB 2; Length 132;

```

Best Local Similarity 30.8%; Pred. No. 0.0018;
Matches 44; Conservative 17; Mismatches 47; Indels 35; Gaps 9;

QY 12 VHPGSCALW-----VSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTWFRD 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 LHVSLVFLWLQGGVSSQKQPSLIVPEGAMSLNCSFSDS-----ASQSIWYQQH 58
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 60 VVPQKEVR-----NCTPEFGRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEV 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 --PGKPKALISIFSGNKK--EGELTVLNRASLH---VSLHIKQSPDSAVILCAVR 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 113 LGLGVGT---GNGLRLVVEKEHP 132
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 SGANTGKLTFGHGILRV---HP 132
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 3
S26408
T-cell receptor beta chain V region (5.5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26408
R:Bowman, S.J.; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A:Description: T cell receptor beta chain sequences from patients with rheumatoid arthritis
A:Reference number: S26408
A:Accession: S26408
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <BW>
A:Cross-references: EMBL:X68527; NID:g36172; PIDN:CAA48540.1; PID:g36173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
P:35-112/Domain: immunoglobulin homology <IMV>

Query Match 11.4%; Score 116; DB 2; Length 146;
Best Local Similarity 26.5%; Pred. No. 0.0027;
Matches 39; Conservative 26; Mismatches 52; Indels 30; Gaps 7;

QY 1 MAWMLLLILIMVHPGSCALWVSQPE--IRTEGSSAFPCSFNASQGRLAIGSVTWFRD 58
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LCWLCLL---GAGSVETGVTQSPHTLTKT-RQQVTLRCSSQSGH-----NTVSWYQQ 56
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRV 110
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 ALGQGPQFIQYRYEEENG-----KGNPPFRSGLQFFNYSELNVNALELDDSDALYLCA 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 111 EVLGLGVGT-----GNGLRLVVEKE 130
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 113 SPKGLGLPSRCGYEQYFGFGITLTVED 139
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
S25756
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25756
R:Combariato, G.; Kiobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25756
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-232 <COM>
A:Cross-references: EMBL:X57821; NID:g33741; PIDN:CAA40958.1; PID:g33742
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
P:147-215/Domain: immunoglobulin homology <IMV>

Query Match 11.3%; Score 115.5; DB 2; Length 232;
Best Local Similarity 26.3%; Pred. No. 0.005;

```

```

Matches 46; Conservative 24; Mismatches 62; Indels 43; Gaps 8;

QY 1 MAWMLLLILIMVH-PGSCALWV-SQPPEIRTEGSSAFPCSFNASQGRLAIGSVTWFRD 58
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAWTLGLLGLSHCTGTSVTLTQPPSVVAPGKTAISITCGGN-----NIGSKSVHYQQ 56
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 59 EVVPGK-----EVRNGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDSIYV 107
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 57 K-PQAPVLVVYDDSDRPSGIPERFSGSNS-----GNTATLTSRVEAGDEADYY 105
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 108 CRVEVLGLGVGTGNTRLVW-----EKHPQLGAGTVLLLRAGFY 147
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 CQWDSSSDVVRGGTKTLVLGQKAPSVTLFPSPSEELQANKATLVCLISDFY 160
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
A46477
membrane-bound immunoglobulin Ig-alpha chain precursor - human
N:Alternate names: B-cell antigen receptor complex alpha chain CD79a; IgM-alpha; immunog
C:Species: Homo sapiens (man)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: I54539; A46477; A49135; A46479; I54496; I57851; S51113
R:Hashimoto, S.; Mohrenweiser, H.W.; Gregersen, P.K.; Chiorazzi, N.
Immunogenetics 40, 287-295, 1994
A:Title: Chromosomal localization, genomic structure, and allelic polymorphism of the hu
A:Reference number: I54539; MUID:94364636; PMID:7916003
A:Accession: I54539
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <HASL>
A:Cross-references: UNIPROT:P11912; GB:L32754; NID:g600875; PIDN:AAA57274.1; PID:g602606
R:Yu, L.M.; Chang, T.W.
J. Immunol. 148, 633-637, 1992
A:Title: Human mb-1 gene: complete cDNA sequence and its expression in B cells bearing m
A:Reference number: A46477; MUID:92105765; PMID:1729378
A:Accession: A46477
A:Molecule type: mRNA
A:Residues: 1-226 <YU>
A:Cross-references: GB:S75217; NID:g241773; PIDN:AA20812.1; PID:g241774
A>Note: sequence extracted from NCBI backbone (NCBIN:75217, NCBI:P:75218)
R:Leduc, I.; Preud'homme, J.L.; Cogne, M.
Clin. Exp. Immunol. 90, 141-146, 1992
A:Title: Structure and expression of the mb-1 transcript in human lymphoid cells.
A:Reference number: A49135; MUID:93009083; PMID:1395095
A:Accession: A49135
A:Molecule type: mRNA
A:Residues: 1-226 <LED>
A:Cross-references: GB:S46706; NID:g257140; PIDN:AA233558.1; PID:g257141
A:Experimental source: Ly66 cell line
A>Note: sequence extracted from NCBI backbone (NCBIN:115213, NCBI:P:115214)
R:Ha, H.J.; Kubagawa, H.; Burrows, P.D.
J. Immunol. 148, 1526-1531, 1992
A:Title: Molecular cloning and expression pattern of a human gene homologous to the muri
A:Reference number: A46479; MUID:92166394; PMID:1538135
A:Accession: A46479
A:Molecule type: mRNA
A:Residues: 1-226 <HA>
A:Cross-references: GB:U05259; NID:g452561; PIDN:AAA20495.1; PID:g521105; GB:M86921; NID
R:Flaswinkel, H.; Reth, M.
Immunogenetics 36, 266-269, 1992
A:Title: Molecular cloning of the Ig-alpha subunit of the human B-cell antigen receptor
A:Reference number: I54496; MUID:92347937; PMID:1639443
A:Accession: I54496
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-69, 170-226 <FLA>
A:Cross-references: GB:M74721; NID:g337419; PIDN:AAA60270.1; PID:g337420
R:Hashimoto, S.; Chiorazzi, N.; Gregersen, P.K.
Mol. Immunol. 32, 651-659, 1995
A:Title: Alternative splicing of CD79a (Ig-alpha/mb-1) and CD79b (Ig-beta/B29) RNA trans
A:Reference number: I57851; MUID:95371688; PMID:7643857
A:Accession: I57851

```



A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-88, 'E', 128-226 <HAS>  
A;Cross-references: GB:979248; NID:91087006; PIDN:AA60653.1; PID:91087007  
submitted to the EMBL Data Library, December 1994  
A;Reference number: S51112  
A;Accession: S51113  
A;Molecule type: mRNA  
A;Residues: 1-88, 'E', 128-226 <KOY>  
A;Cross-references: EMBL:X83540; NID:9620080; PIDN:CAA58523.1; PID:9620081  
C;Genetics:  
A;Gene: GDB:IGA; mb-1; CD79a  
A;Cross-references: GDB:133778; OMIM:600352  
A;Map position: 19q13.2-19q13.2  
A;Introns: 27/1; 127/1; 166/3; 190/1  
C;Complex: disulfide-linked heterodimer with Ig-beta; heterodimer associates non-covalently with Ig-alpha chain #status predicted <SIG>  
C;Keywords: alternative splicing; disulfide bond; glycoprotein; immunoglobulin; surface Fc; 3-226/Domain: signal sequence #status predicted <SIG>  
F;33-226/Product: membrane-bound immunoglobulin Ig-alpha chain #status predicted <EXT>  
F;33-143/Domain: extracellular #status predicted <EXT>  
F;144-165/Domain: transmembrane #status predicted <TM>  
F;166-226/Domain: intracellular #status predicted <CYT>  
F;57,63,73,88,97,112/Binding site: carbohydrate (asn) (covalent) #status predicted  
F;57,63,73,88,97,112/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 10.9%; Score 111.5; DB 2; Length 226;  
Best Local Similarity 28.0%; Pred. No. 0.011;  
Matches 47; Conservative 24; Mismatches 70; Indels 27; Gaps 8;

QY 4 MLLILIMVPGSCALVSO-PPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVP 62  
Db 18 LFLSAYVLGPGCOALMHWKVPASLVSLGDAHFQCPHNSNN-ANVTWVR-VLH 71  
QY 63 GKEVRNGT-PEFGRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVCRVEVLGLGVGTG 120  
Db 72 G---NVTWPDEFGLP-----GDPNGTLIIQNVKSHGSIYVCRVQEGNESYQOS 118  
QY 121 NGTPLVVEKEHPQ---LGRGTV-LLLRAGFYAVSFLSVAGSVTVYQ 163  
Db 119 CGTYLRVQPPRFLDMGEGTKNRITAEGIILLFCVAVPGTLLFLR 166

RESULT 6  
S25747  
Ig lambda chain - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S25747  
R;Combrinato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda  
A;Reference number: S16439; MUID:91257162; PMID:1904362  
A;Accession: S25747  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-233 <COM>  
A;Cross-references: EMBL:X57812; NID:9337723; PIDN:CAA04949.1; PID:933724  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;148-216/Domain: immunoglobulin homology <IMV>

Query Match 10.9%; Score 111; DB 2; Length 233;  
Best Local Similarity 28.0%; Pred. No. 0.013;  
Matches 49; Conservative 24; Mismatches 60; Indels 42; Gaps 10;

QY 1 MAWMLLLIMVH-PGSCALVW-SOPPIRTLEGSSAFPLPCSFNASQGRLAIGSVTWFR 57  
Db 1 MAWTVLLGLLSHCSTSVTSYVLTQPPSVAPGAARITCG-----GINASKSVHWV 55  
QY 58 DB-----VVPGEKVR-NGTPE-FRGLAPLASSRFLHDHQAELHIRDVRGHDSIYVC 108  
Db 56 QKPGQAPVLVYVYGDSRPSGIPERFSGNS-----GNTATLINISRVAGDEAAVYC 106

QY 109 RV-EVLGLVGTGNGTRLVV-----EKEHPOLGAGTVLLLRAGFY 147  
Db 107 QWMDSSDHVYVFGGKTITVLGQPKAAPSVTLFPPSSEELQANKATILVCLISDFY 161

RESULT 7  
T09536  
cytotoxic T-lymphocyte protein 4 - human  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C;Accession: T09536  
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.  
J. Immunol. 147, 1037-1044, 1991  
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou  
A;Reference number: 149584; MUID:91318145; PMID:1713603  
A;Accession: T09536  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-223 <HAR>  
A;Cross-references: EMBL:L15006; NID:9291928; PIDN:AAB59385.1; PID:9291929  
C;Genetics:  
A;Gene: CTLA4  
A;Map position: 2q33  
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C;Keywords: T-cell; transmembrane protein

Query Match 10.8%; Score 110; DB 2; Length 223;  
Best Local Similarity 28.0%; Pred. No. 0.015;  
Matches 47; Conservative 22; Mismatches 75; Indels 24; Gaps 6;

QY 6 LLLILIMVPGSC-ALWVSPQPEIRTEGSSAFPLPCSFNASQGRLAIGSVTWFRDEVVP 64  
Db 24 LFLFLLFIPVFCAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLROADSQVT 82  
QY 65 EYRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDSIYVCRVEVL-- 113  
Db 83 EYCAATYMTGNELT-----FLDDSICTGSSGNVLTIQGLRAMDTGLYICKVELMYP 136  
QY 114 -GLGVGTGNGTRLVVEKEHPOLGAGTVLLLR-----GFYAVSFLSVAV 156  
Db 137 PYYIGIGNGTQIYVIDPEPCDSDFLLWILAAVSSGLFFYSFLTAV 184

RESULT 8  
A29063  
cytotoxic T-lymphocyte protein 4 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
C;Accession: A29063; 149622  
R;Brunet, J.F.; Denizot, F.; Luciani, M.F.; Roux-Dosseto, M.; Suzan, M.; Mattei, M.G.;  
Nature 328, 267-270, 1987  
A;Title: A new member of the immunoglobulin superfamily--CTLA-4.  
A;Reference number: A29063; MUID:87258259; PMID:3496540  
A;Accession: A29063  
A;Molecule type: mRNA  
A;Residues: 1-223 <BRU>  
A;Cross-references: UNIPROT:P09793; GB:X05719; NID:950592; PIDN:CAA29191.1; PID:950593  
R;Harper, K.; Balzano, C.; Rouvier, E.; Mattei, M.G.; Luciani, M.F.; Golstein, P.  
J. Immunol. 147, 1037-1044, 1991  
A;Title: CTLA-4 and CD28 activated lymphocyte molecules are closely related in both mou  
A;Reference number: 149584; MUID:91318145; PMID:1713603  
A;Accession: 149622  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-36 <RES>  
A;Cross-references: GB:M74362; NID:9192833; PIDN:AAA37489.1; PID:9553903  
C;Genetics:  
A;Gene: Ccla-4  
A;Map position: 1, band C  
C;Superfamily: T-cell surface glycoprotein CD28; immunoglobulin homology  
C;Keywords: transmembrane protein

Query Match 10.6%; Score 108.5; DB 2; Length 223;



F:21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <NAT>  
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match	10.4%;	Score 105.5;	DB 2;	Length 131;
Best Local Similarity	29.6%;	Pred. No. 0.017;		
Matches	37;	Conservative	19;	Mismatches 42;
				Indels 27;
				Gaps 7

Qy	21	VQSPPEIRTL	EGSSAFIP	PCSFN	ASQGR	LAIGSV	TWTF----	RDEV	VPGK	VRNG	TPPR	75
		:	:	:	:	:	:	:	:	:	:	
Db	24	VQSPSALSJL	HEGTSAL	RGNFTT	-----	NR	AVQF	RKNS	RGLN	LYL	ASG	77
		:	:	:	:	:	:	:	:	:	:	
Qy	76	RLAPASSR	FHLDHQA	ELHIRD	VDRGH	DASTY	VVC	REVL	GLG	VG	TG	135
		:	:	:	:	:	:	:	:	:	:	
Db	78	RLKS	AFDSK	--ERY	STLH	IRDA	OLEDS	GT	YFCA	AE-----	STSS	121
		:	:	:	:	:	:	:	:	:	:	
Qy	136	AGTVL	140									
		:	:									
Db	122	OGTIL	126									
		:	:									

```

RESULT 13
RWM5AV
T-cell receptor alpha chain precursor V region (2B4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A02015
R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.
Nature 312, 31-35, 1984
A:title: A third type of murine T-cell receptor gene.
A:Reference number: A93344; MUID:85036634; PMID:8548551
A:Accession: A02015
A:Molecule type: mRNA
A:Residues: 1-132 <CHI>
A:Cross-references: UNIPROT:P01739
A:Experimental source: HybriDoma 2B4, clone Tt11
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: Glycoprotein; heterotrimer; receptor; T-cell
F:1-20/Domain: signal sequence #status Predicted <Sig>
F:21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <Mat>
F:21-113/Region: V segment
F:114-117/Region: D segment
F:118-132/Region: J segment
F:42/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match	10.4%;	Score 106;	DB 1;	Length 132;
Best Local Similarity	25.8%;	Pred. No. 0.019;		
Matches	40;	Conservative 22;	Mismatches 45;	Indels 48; Gaps 9
Qy	3	WMLLILIMVHGSCALWVS-----QPPPIRTLEGGSAFLPCSNASQGRLAGTSVTW	55	
Db	12	WULL-----NWNVSQQNVQSPESLIVPEGARTSLACTFSDASQV----FWW	55	
Qy	56	FRDEVVPGKEVR-----NGTPFPRGRGLAPLASSRFLHDHQAEIHRDVRGHGDSAIYVC	108	
Db	56	YRCH--SGKAPKALMSIFSNGEKE--EGEFTTHINKASLH---PSLIHRQSPDSALSALYIC	109	
Qy	109	RVEVLGLGVGTGNGTRLVWVEKHPOLGAGTVLLIR	143	
Db	110	AVTLVG-----GSGNKLI-----FGTGTLLSVK	132	

RESULT 14  
F45893  
T-cell receptor alpha chain precursor V region (BTA25) - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C/Accession: F45893  
P/Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A/Title: sequence analysis of bovine T-cell receptor alpha chain.  
A/Reference number: A45893; MUID:90129157; PMID:2137108  
A/Accession: F45893  
A/Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-131 <ISH>  
A;Cross-references: GB:D90015; NID:9217618; PI  
C;Superfamily: immunoglobulin V region; immuno  
P:36-109/Domain: immunoglobulin homology <IMM>

Query Match	10.3%;	Score 105;	DB 2;	Length 131;
Best Local Similarity	30.3%;	Pred. No. 0.024;		
Matches	36;	Conservative	23;	Mismatches 34; Indels 26; Gaps 8;
Qy	21	VSQPPETLT-EGSAFLPCSPNASQRLAIGSVTWFRDEVPGKE-----VANGTPEF	73	
Db	24	VEQSPSVLSQEGANSLTRCNFSDT-----VDSQWFQQN--PGGALTTIFFIASGPKK-	75	
Qy	74	RGR LAPLASSRFLHDQAEHLHIDVRGHDAISIVCRVEVLGLVGT-----GNGTRLVW	127	
Db	76	NEWASSMNVK---FRYSTHITATASQEDATVLCVD---IGSGNQLVFGKGTIRLAV	128	

RESULT 15  
S09713  
Ig lambda chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S09713  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains  
A:Reference number: S09710; MUID:90262535; PMID:2111699

A:Accession: S05713  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <HUG>  
A:Cross-references: UNIPROT:Q9N355  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:334-110/Domain: immunoglobulin homology <IMM>

	Query Match	10.2%; Score 104.5; DB 2; Length 132;	
	Best Local Similarity	29.8%; Pred. No. 0.026;	
	Matches	Conservative 20; Mismatches 54; Indels 25; Gaps 8;	
Qy	1 MAWMLLLILIMVH-PGSCALMV-SOPEIRTELGSSAFLPCSFNWSQRLAIGSVTFRD	58	
	:    :    :    :    :    :		
Dd	1 MAWTVLLGLLSHTGVTSYVLTPPPSVSVAPQTARITC- <del>CGTENNIGRKSVHWIQ</del>	58	
	:    :    :    :    :    :		
Qy	59 E-----VVPGKEVR-NGTIPE-FGRGLAPIASSRFLHDHQAEHLIRDVRGHDSIYYCR	109	
	:    :    :    :    :    :		
Dd	59 KFGQAPLVIVYGASDRPSGPIPERSGNS-----GNTATLITISRVAGDEADYYCQ	109	
	:    :    :    :    :    :		
Qy	110 V---EVLGLVGVTGNGTRLVV	127	
	:    :    :    :    :		
Dd	110 VWDSSSAHPGVVVFGGTKLTIV	130	
	:    :    :    :    :		

Search completed: November 16, 2004, 19:15:51  
Job time : 41.3103 secs

F;21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <MAT>  
F;36-109/Domain: immunoglobulin homology <IMM>

Query Match	10.4%;	Score 105.5;	DB 2;	Length 131;
Best Local Similarity	29.6%;	Pred. No. 0.017;		
Matches	37;	Conservative	19;	Mismatches 42;
				Indels 27;
				Gaps 7

Qy	21	VSQPPEIRTL-EGSSAFILPCSFNAGSQRLLAIGSVTWTF-----RDEVVPGKVRNGNPERRG	75
Dd	24	VQSFSASJLHSGTGSAIRCNTFTT-----NRVQMFRKNRGSLINLYLASGTKE-NG	77
Qy	76	RLIAPASSRFHLHDQAEHLIRDVRGHDASTIVCVREVLGVGTGNTRLVWEKEHPQG	135
Dd	78	RLKSADFSGK--ERYSTLIHRDAOLEDSGTYFCAAE-----STSSGQKLIV-----FG	121
Qy	136	AGTVL 140    :	
Dd	122	OGTIL 126    :	

```

RESULT 13
RWM5AV
T-cell receptor alpha chain precursor V region (2B4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A02015
R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.
Nature 312, 31-35, 1984
A:title: A third type of murine T-cell receptor gene.
A:Reference number: A93344; MUID:85036634; PMID:8548551
A:Accession: A02015
A:Molecule type: mRNA
A:Residues: 1-132 <CHI>
A:Cross-references: UNIPROT:P01739
A:Experimental source: HybriDoma 2B4, clone Tt11
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; receptor; T-cell
F:1-20/Domain: signal sequence #status Predicted <Sig>
F:21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <Mat>
F:21-113/Region: V segment
F:114-117/Region: D segment
F:118-132/Region: J segment
F:42/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match	10.4%;	Score 106;	DB 1;	Length 132;
Best Local Similarity	25.8%;	Pred. No. 0.019;		
Matches	40;	Conservative 22;	Mismatches 45;	Indels 48; Gaps 9
Qy	3	WMLLILIMVHGSCALMVS-----QPPPIRTLEGSSAFLLPCSNASQGRLAIGSVTM	55	
Db	12	WULL-----NMVNSQQNVQSPESLIVPEGARTSLACTFSDASQV----	FWM	55
Qy	56	FRDEVVPGKEVR-----NGTPFPRGRAPLASSRFLHDHQAEIIRDIVRGCHDASIYVC	108	
Db	56	YRCH--SGKAPKALMSIFSNGEKE--EGEFTTHINKASLH---PSLIHRQSPDSALYLC	109	
Qy	109	RVEVLGLVGTGNGTRLVVEKEHPOLGAGTVLLIR	143	
Db	110	AVTLVG-----GSGNKLI-----FGTGTLLSVK	132	

RESULT 14  
F45893  
T-cell receptor alpha chain precursor V region (BT425) - bovine  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C/Accession: F45893  
P/Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A/Title: sequence analysis of bovine T-cell receptor alpha chain.  
A/Reference number: A45893; MUID:90129157; PMID:2137108  
A/Accession: F45893  
A/Status: preliminary

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 202.095 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: us-10-036-444-2

Perfect score: 1020

Sequence: 1 MAWMLLLILIMVHPGSCALW.....GTHCHSDGPRGVPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	190	AAE02769	Aae02769 Human Nkp
2	1020	100.0	190	ADO19810	Ado19810 Human Nkp
3	1020	100.0	190	ADQ30923	Adq30923 Human Nkp
4	1018	99.8	190	Aay06401	Aay06401 Human B-c
5	876	85.9	201	2 AAY06403	Aay06403 Human B-c
6	859	84.2	177	2 AAY06402	Aay06402 Human B-c
7	713	69.9	135	5 AAE19109	Aae19109 Human Nkp
8	713	69.9	369	5 AAE19110	Aae19110 Human Nkp
9	632	62.0	120	8 AAE02771	Aae02771 Human Nkp
10	632	62.0	120	8 ADQ30924	Adq30924 Human Nkp
11	608.5	59.7	382	8 ADP48750	Adp48750 Human Nkp
12	204	20.0	33	8 AAE02773	Aae02773 Human Nkp
13	204	20.0	33	8 ADQ30926	Adq30926 Human Nkp
14	123.5	12.1	246	5 AAE02073	Aae02073 Human lun
15	119.5	11.7	232	6 ABU08020	Abu08020 Monoclonal
16	119.5	11.7	232	7 ADF5784	Adf5784 Human ant
17	119.5	11.7	232	8 ADJ92520	Adj92520 Human SOU
18	118.5	11.6	139	5 AAU75565	Aau75565 Murine T
19	118.5	11.6	212	2 AAR60134	Aar60134 CTLA4 rec
20	118.5	11.6	212	2 AAR77642	Aar77642 Full leng
21	118.5	11.6	212	2 AAY43479	Aay43479 Amino aci
22	118.5	11.6	212	2 AAW81584	Aaw81584 Human CTL
23	118.5	11.6	212	2 ABB78106	Abb78106 Amino aci
24	118.5	11.6	212	5 AAU75124	Aau75124 Human CTL
25	118.5	11.6	212	5 AAU75132	Aau75132 Human CTL

26	118.5	11.6	212	6 ABP56715	Abp56715 Human CTL
27	118.5	11.6	212	7 ADD89013	Add89013 CTLA4 rec
28	116.5	11.4	212	5 AAU75126	Aau75126 Human CTL
29	116	11.4	211	5 AAW87560	Aaw87560 Human CTL
30	115.5	11.3	212	5 AAU75127	Aau75127 Human CTL
31	115.5	11.3	212	5 AAU75131	Aau75131 Human CTL
32	115.5	11.3	212	5 AAU75130	Aau75130 Human CTL
33	114.5	11.2	212	5 AAU75133	Aau75133 Human CTL
34	112	11.0	222	6 ABP59948	Abp59948 Human CTL
35	112	11.0	223	3 AAY15129	Aay15129 Human cyt
36	112	11.0	223	5 AAU74509	Aau74509 Human cyt
37	112	11.0	223	5 AAU74508	Aau74508 Human cyt
38	112	11.0	223	8 ADP12469	Adp12469 Protein e
39	112	11.0	235	4 AAG64474	Aag64474 Human typ
40	112	11.0	700	8 ADN14450	Adn14450 Mouse dop
41	111.5	10.9	212	2 AAR31040	Aar31040 Human CTL
42	111.5	10.9	212	5 AAU75129	Aau75129 Human CTL
43	111.5	10.9	226	2 AAR24112	Aar24112 Human mb-
44	111.5	10.9	226	3 AAY52553	Aay52553 Human mb-
45	111.5	10.9	226	6 ABG74347	Abg74347 Human Iga

## ALIGNMENTS

RESULT 1  
AAE02769  
ID AAE02769 standard; protein; 190 AA.

AC AAE02769;

XX 06-AUG-2001 (first entry)

XX Human Nkp30 receptor.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
XX melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
XX immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
XX therapy.

XX Homo sapiens.

XX Location/Qualifiers

FT Key

FT Peptide

FT Protein

FT Region

FT Modified-site

FT Modified-site

FT Region

FT Region

FT Region

FT Region

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DR WPI; 2001-329221/34.  
 XX N-PSDB; AAD06564.  
 PT Novel compound, useful for detection and/or quantifying the presence of  
 PT NK cells, comprises the amino acid sequences of the NKp30 molecule.  
 XX  
 XX  
 PS Claim 1; Fig 7B; 83pp; English.  
 XX  
 CC The invention relates to human NKp30 receptor and its corresponding cDNA  
 CC molecule which is involved in natural cytotoxicity mediated by natural  
 CC killer (NK) cells and antibodies that identify the same. NKp30 receptor  
 CC is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively  
 CC expressed on the surface of human mature NK cells. NKp30 and its cDNA are  
 CC useful for detecting and/or quantifying the presence of NK cells in a  
 CC biological sample. The invention also provide kits for detecting and/or  
 CC quantifying the presence of NK cells, for the selective removal of NK  
 CC cells from a biological sample, for the positive and selective  
 CC purification of NK cells from a biological sample and for the in vitro  
 CC stimulation of NK cell cytotoxicity. The invention further provides a  
 CC pharmaceutical composition which is used as a drug for grafting  
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
 CC the prevention, palliation and/or therapy of solid or liquid tumours,  
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 CC microorganism, notably viral infection. NKp30 antibodies are useful for  
 CC identifying NKp30 natural ligands and allow assessment of the level of  
 CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
 CC comparison of this level to the standard physiological one. Hence NKp30  
 CC antibodies are useful in the diagnosis of tumours or of infection. The  
 CC present sequence is human NKp30 receptor  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 1020; DB 4; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-92;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDEV 60  
 DB 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDEV 60  
 QY 61 VPGKEVNGTPEFGRGLAPLASSRFLHDQAEHLHIDVRGHDASIVYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVNGTPEFGRGLAPLASSRFLHDQAEHLHIDVRGHDASIVYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFVLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFVLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 QY 181 RGVIPEPRCP 190  
 DB 181 RGVIPEPRCP 190  
 RESULT 2  
 AD019810  
 ID AD019810 standard; protein; 190 AA.  
 AC AD019810;  
 XX  
 DT 12-AUG-2004 (first entry)  
 XX  
 DE Human PRO polypeptide #367.  
 XX  
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;  
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;  
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX

OS Homo sapiens.  
 XX  
 FN WO2004043361-A2.  
 XX  
 PD 27-MAY-2004.  
 XX  
 XX  
 FF 06-NOV-2003; 2003WO-US035268.  
 XX  
 XX 08-NOV-2002; 2002US-0425235P.  
 XX (GETH) GENENTECH INC.  
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 PI Wood WI, Wu TD;  
 XX WPI; 2004-420067/39.  
 DR N-PSDB; ADO19809.  
 XX  
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 PT treating an immune related disorder such as systemic lupus erythematosus,  
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 PT spondyloarthritis.  
 XX  
 PS Claim 7; SEQ ID NO 734; 1731pp; English.  
 XX  
 CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, diabetes  
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.  
 XX  
 SQ Sequence 190 AA;  
 Query Match 100.0%; Score 1020; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-92;  
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDEV 60  
 DB 1 MAMWLLILIMVHPGSCALWVSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFDRDEV 60  
 QY 61 VPGKEVNGTPEFGRGLAPLASSRFLHDQAEHLHIDVRGHDASIVYCRVEVLGLGVGTG 120  
 DB 61 VPGKEVNGTPEFGRGLAPLASSRFLHDQAEHLHIDVRGHDASIVYCRVEVLGLGVGTG 120  
 QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFVLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFVLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180  
 QY 181 RGVIPEPRCP 190  
 DB 181 RGVIPEPRCP 190  
 RESULT 3  
 ADQ30923  
 ID ADQ30923 standard; protein; 190 AA.  
 AC ADQ30923;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human NKp30 polypeptide.  
 XX  
 KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
 XX

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OS Homo sapiens.
XX Key Location/Qualifiers
FH Region 19..138
FT /label= Extracellular region
FT /notes= "Region specifically described in Claim 3"
FT Region 20..133
FT /label
FT /notes= "Immunogenic peptide specifically described in
FT Claim 3"
FT Region 139..157
FT /label= Transmembrane region
FT /notes= "Region specifically described in Claim 3"
FT Region 158..190
FT /label= Cytoplasmic tail
FT /notes= "Region specifically described in Claim 3"
XX WO2004056392-A1.
XX PN
XX FN
XX PD 08-JUL-2004.
XX PF 22-DEC-2003; 2003WO-EP014716.
XX PR 23-DEC-2002; 2002US-0435344P.
XX PA (INNA-) INNATE PHARMA.
XX PI Romagne F, Andre P;
XX WPI; 2004-507595/48.
XX
XX Pharmaceutical compositions that stimulate proliferation of natural
XX killer cells useful for therapy of melanoma, chronic myeloid, and
XX leukemia, comprise an anti-natural killer cell receptor antibody and
XX interleukins.
XX Claim 3; SEQ ID NO 1; 35pp; English.
XX
XX The present sequence is that of human Nkp30, a 190 amino acid polypeptide
XX (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
XX killer (NK) cells, and particularly by mature NK cells. Claimed
XX pharmaceutical compositions that have a stimulating effect on the
XX proliferation of NK cells comprise an antibody such as an anti-Nkp30
XX antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
XX antibody(ies) and cytokine(s) being administered together or separately
XX to a subject. The anti-Nkp30 antibody is an isolated antibody or its
XX antigen-binding fragment which specifically binds to Nkp30 or to a
XX fragment ADQ30924-ADQ30927 of Nkp30. The pharmaceutical compositions,
XX when used for daily subcutaneous injection, comprising from 1 ng to 100
XX mg/kg (body weight) of antibody(ies), and lower than 1 million
XX units/square meters/day of cytokine(s), are useful for the prevention,
XX palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
XX myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
XX adenocarcinoma, neuroblastoma and for antimicrobial prevention,
XX palliation and therapy (claimed).
XX Sequence 190 AA;
XX
XX Query Match 100.0%; Score 1020; DB 8; Length 190;
XX Best Local Similarity 100.0%; Pred. No. 8,3e-92;
XX Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
XX Db
XX 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEV 60
XX
XX 61 VPGKEVRNGTPEFFGRGLAPLASSFLHDHQAELHIRDVRGHDAISIVCRVEVLGLGVGTG 120
XX Qy
XX 61 VPGKEVRNGTPEFFGRGLAPLASSFLHDHQAELHIRDVRGHDAISIVCRVEVLGLGVGTG 120
XX Db
XX 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
XX Qy

```

```

Db 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVYQKCHCHMGTHCHSSDGP 180
Qy 181 RGVIPERPCP 190
Db 181 RGVIPERPCP 190
RESULT 4
AAV06401
ID AAV06401 standard; protein; 190 AA.
XX
XX AAY06401;
XX 20-SEP-1999 (first entry)
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX signal transduction; immunomodulator; anti-inflammatory;
XX autoimmune disease; inflammation; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..12
FT /note= "leader peptide"
FT Protein 13..190
FT /note= "mature protein"
FT Modified-site 42
FT /note= "N-glycosylated"
FT Modified-site 58
FT /note= "N-glycosylated"
FT Modified-site 121
FT /note= "N-glycosylated"
FT Domain 139..162
FT /note= "transmembrane domain"
FT Peptide 166..190
FT /note= "alternatively spliced C-terminal end"
XX
XX WO9923867-A2.
XX
XX 20-MAY-1999.
XX
XX 05-NOV-1998; 98WO-US023826.
XX
XX 07-NOV-1997; 97US-0064761P.
XX (BIOJ ) BIOGEN INC.
XX
XX Browning J;
XX
XX WPI; 1999-418423/35.
XX N-PSDB; AAX59347.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
XX
XX Claim 2; Page 42; 43pp; English.
XX
XX This sequence represents human BMOG, a novel member of the B cell myelin
XX oligodendrocyte glycoprotein family that is expressed by germinal centre
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
XX identified. The protein is present primarily in the spleen, in lymph
XX nodes and in germinal centre B cells. It may have immunoregulatory
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to
XX regulate the immune system in autoimmune or inflammatory disease. Vectors
XX comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
XX producing BMOG using these transformed host cells are also provided. BMOG
XX polypeptides can be used for modulating the immune system of a subject or
XX to inhibit signal transduction in a cell expressing BMOG by contacting it
XX with a soluble BMOG protein. The nucleic acid can be used for gene
XX therapy. The protein can also be used to target a toxin, imaging agent or
XX radionuclide to a cell expressing BMOG. (All claimed)
XX

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SQ Sequence 190 AA;
Query Match 99.8%; Score 1018; DB 2; Length 190;
Best Local Similarity 99.5%; Pred. No. 1.3e-91;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGGSAFLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGGSAFLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAVGSTVYVYQKCHMGTHCHSSDGP 180
DB 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAVGSTVYVYQKCHMGTHCHSSDGP 180
QY 181 RGVIPERCP 190
DB 181 RGVIPERCP 190

RESULT 5
AA06403
ID AA06403 standard; protein; 201 AA.
XX AC AA06403;
XX DT 20-SEP-1999 (first entry)
XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX KW signal transduction; immunomodulator; antiinflammatory;
XX KW autoimmune disease; inflammation; gene therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..12
XX FT Protein /note= "leader peptide"
XX FT Modified-site 42
XX FT Modified-site /note= "mature protein"
XX FT Modified-site /note= "N-glycosylated"
XX FT Modified-site /note= "N-glycosylated"
XX FT Domain 121
XX FT Domain 139..162
XX FT Peptide /note= "transmembrane domain"
XX FT Peptide 166..201
XX FT /note= "alternatively spliced C-terminal end"
XX PN WO9923867-A2.
XX PD 20-MAY-1999.
XX PF 05-NOV-1998; 96WO-US023926.
XX PR 07-NOV-1997; 97US-0064761P.
XX PA (BIOJ ) BIOGEN INC.
XX PI Browning J;
XX DR WPI; 1999-418423/35.
XX DR N-PSDB; AAX59349.
XX PT Novel B-cell myelin oligodendrocyte glycoproteins.
XX PS Claim 2; Page 43; 43pp; English.

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This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AA06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)

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XX Sequence 201 AA;
Query Match 85.9%; Score 876; DB 2; Length 201;
Best Local Similarity 89.2%; Pred. No. 1.2e-77;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;
QY 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGGSAFLPCSFNASQGRLAIGSVTWRDEV 60
DB 1 MAWMLLLILIMVHPGSCALWVSQPEIRTLGGSAFLPCSFNASQGRLAIGSVTWRDEV 60
QY 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGRPLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAVGSTVYVYQKCHMGTHCHSSDGP 180
DB 121 NGTRLVWEKEHPQAGTIVLLLRAGFYAVSFLSVAVGSTVYVYQKCHMGTHCHSSDGP 180
QY 181 R---GVIPERCP 190
DB 173 RRLPVAVPAPLPP 186

RESULT 6
AA06402
ID AA06402 standard; protein; 177 AA.
XX AC AA06402;
XX DT 20-SEP-1999 (first entry)
XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX KW signal transduction; immunomodulator; antiinflammatory;
XX KW autoimmune disease; inflammation; gene therapy; diagnosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..12
XX FT Protein /note= "leader peptide"
XX FT Modified-site 42
XX FT Modified-site /note= "mature protein"
XX FT Modified-site /note= "N-glycosylated"
XX FT Modified-site /note= "N-glycosylated"
XX FT Modified-site /note= "N-glycosylated"
XX FT Domain 139..162
XX FT Peptide /note= "transmembrane domain"
XX FT Peptide 166..177
XX PN WO9923867-A2.

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PD 20-MAY-1999.  
XX 05-NOV-1998; 98WO-US023826.  
PF 07-NOV-1997; 97US-0064761P.  
XX (BIOJ ) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
DR N-PSDB; AAX59348.  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX Claim 2; Page 43; 43pp; English.  
XX This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAI06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)  
XX SQ Sequence 177 AA;  
Query Match 84.2%; Score 859; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.9e-76;  
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEV 60  
DB 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEV 60  
QY 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120  
DB 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120  
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVQCK 165  
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYVQCK 165  
RESULT 7  
AAE19109  
ID AAE19109 standard; protein; 135 AA.  
XX AAE19109;  
AC AAE19109;  
DT 21-MAY-2002 (first entry)  
XX Human Nkp30 protein.  
XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;  
KW viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;  
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; Nkp30.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200208287-A2.  
XX 31-JAN-2002.  
XX 19-JUL-2001; 2001WO-IL000664.

PR 20-JUL-2000; 2000IL-00137419.  
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (UYNE ) UNIV BEN-GURION NEGEV.  
XX Mandelboim O, Porgador A;  
XX WPI; 2002-195870/25.  
DR N-PSDB; AAD30466.  
XX New targeting complex capable of targeting an active substance to a target cell, comprising a target recognition segment and an active segment, useful for treating pathologies associated with viral infections or cancer.  
XX Example 1; Page 108; 113pp; English.  
XX The invention relates to compositions and methods for the treatment and detection of a variety of viral infections, by using complex agents comprising the natural killer (NK) cells activating proteins, Nkp46 and Nkp44 and functional fragments thereof, linked to therapeutic or imaging agents. The complex is useful for treating pathologies associated with viral infections (e.g. infections caused by influenza virus, HIV, Epstein-Barr virus, cytomegalovirus, vaccinia virus, ECWV, MVM or herpes virus) and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for the imaging and monitoring of cancer. The complex may also be used to detect the presence of abnormal cells in a sample. The antibodies can be used to qualitatively or quantitatively detect the ligand for the complex. The present sequence is human Nkp30 protein  
XX SQ Sequence 135 AA;  
Query Match 69.9%; Score 713; DB 5; Length 135;  
Best Local Similarity 100.0%; Pred. No. 7.6e-62;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEV 60  
DB 1 MAWMLLLILIMVHPGSCALWVSQPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTFRDEV 60  
QY 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120  
DB 61 VPGKEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120  
QY 121 NGTRLVVEKEHPQLG 135  
DB 121 NGTRLVVEKEHPQLG 135  
RESULT 8  
AAE19110  
ID AAE19110 standard; protein; 369 AA.  
XX AAE19110;  
AC AAE19110;  
DT 29-AUG-2003 (revised)  
DT 21-MAY-2002 (first entry)  
XX Human Nkp30-IgG fusion protein.  
XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;  
KW viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;  
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;  
KW immunoglobulin G; fusion protein.  
XX Homo sapiens.  
OS Homo sapiens.  
XX Chimeric.  
XX Key Location/Qualifiers  
FT Region 1..135 /note= "Human Nkp30"  
FT Region 136..369 /note= "Human IgG"  
FT FT

XX PN WO200208287-A2.  
 XX PD 31-JAN-2002.  
 XX PF 19-JUL-2001; 2001WO-IL000664.  
 XX PR 20-JUL-2000; 2000IL-00137419.  
 XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX PA (UYNE ) UNIV BEN-GURION NEGEV.  
 XX PI Mandelboim O, Porgador A;  
 XX WI; 2002-195870/25.  
 XX DR N-PSDB; AAD30467.  
 XX PS New targeting complex capable of targeting an active substance to a  
 PT target cell, comprising a target recognition segment and an active  
 PT segment, useful for treating pathologies associated with viral infections  
 PT or cancer.  
 XX PS Example 1; Page 108-110; 113pp; English.  
 XX CC The invention relates to compositions and methods for the treatment and  
 CC detection of a variety of viral infections, by using complex agents  
 CC comprising the natural killer (NK) cells activating proteins, Nkp46 and  
 CC Nkp44 and functional fragments thereof, linked to therapeutic or imaging  
 CC agents. The complex is useful for treating pathologies associated with  
 CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
 CC Barr virus, cytomegalovirus, vaccinia virus, ECV, MVM or herpes virus)  
 CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
 CC the imaging and monitoring of cancer. The complex may also be used to  
 CC detect the presence of abnormal cells in a sample. The antibodies can be  
 CC used to qualitatively or quantitatively detect the ligand for the  
 CC complex. The present sequence is human Nkp30- immunoglobulin G (IgG) Fc  
 CC region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)  
 XX CC Sequence 369 AA;  
 PS Query Match 69.9%; Score 713; DB 5; Length 369;  
 CC Best Local Similarity 100.0%; Pred. No. 2.8e-61;  
 CC Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MAWMLLLILMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEV 60  
 DB 1 MAWMLLLILMVHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEV 60  
 QY 61 VPKQEVNRTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
 DB 61 VPKQEVNRTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
 QY 121 NGTFLVVEKEHPOLG 135  
 DB 121 NGTFLVVEKEHPOLG 135  
 RESULT 9  
 AA02771  
 ID AAE02771 standard; protein; 120 AA.  
 AC AA02771;  
 XX DT 06-AUG-2001 (first entry)  
 XX DE Human Nkp30 receptor extracellular region sequence.  
 DE Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
 KW therapy; extracellular region.  
 XX Homo sapiens.  
 OS

XX PN WO200136630-A2.  
 XX PD 25-MAY-2001.  
 XX PF 15-NOV-2000; 2000WO-EP011697.  
 XX PR 15-NOV-1993; 99CA-02288307.  
 XX PR 15-NOV-1993; 99US-00440514.  
 XX PA (INNA-) INNATE PHARMA SAS.  
 XX PA (UYGE-) UNIV GENOVA.  
 XX PI Moretta A, Bottino C, Blassoni R;  
 XX WI; 2001-329221/34.  
 XX DR  
 XX PS Novel compound, useful for detection and/or quantifying the presence of  
 PT NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
 XX PS Claim 1; Fig 7B; 83pp; English.  
 XX CC The invention relates to human Nkp30 receptor and its corresponding cDNA  
 CC molecule which is involved in natural cytotoxicity mediated by natural  
 CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
 CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
 CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
 CC useful for detecting and/or quantifying the presence of NK cells in a  
 CC biological sample. The invention also provide kits for detecting and/or  
 CC quantifying the presence of NK cells, for the selective removal of NK  
 CC cells from a biological sample, for the positive and selective  
 CC purification of NK cells from a biological sample and for the in vitro  
 CC stimulation of NK cell cytotoxicity. The invention further provides a  
 CC pharmaceutical composition which is used as a drug for grafting  
 CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
 CC the prevention, palliation and/or therapy of solid or liquid tumours,  
 CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
 CC identifying Nkp30 natural ligands and allow assessment of the level of  
 CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
 CC comparison of this level to the standard physiological one. Hence Nkp30  
 CC antibodies are useful in the diagnosis of tumours or of infection. The  
 CC present sequence is the extracellular region of human Nkp30 receptor  
 XX CC Sequence 120 AA;  
 PS Query Match 62.0%; Score 632; DB 4; Length 120;  
 CC Best Local Similarity 100.0%; Pred. No. 5.9e-54;  
 CC Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 19 LWVSQPPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEVVPGKEVRNGTPEFRGLA 78  
 DB 1 LWVSQPPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTWFREDEVVPGKEVRNGTPEFRGLA 60  
 QY 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTFLVVEKEHPOLGAGT 138  
 DB 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTFLVVEKEHPOLGAGT 120  
 RESULT 10  
 ADQ30924  
 ID ADQ30924 standard; protein; 120 AA.  
 XX AC ADQ30924;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Human Nkp30 extracellular region.  
 XX DE Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.  
 XX Homo sapiens.  
 OS

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XX PN WO2004056392-A1.
XX PD 08-JUL-2004.
XX PF 22-DEC-2003; 2003WO-EP014716.
XX PR 23-DEC-2002; 2002US-0435344P.
XX PA (INNA-) INNATE PHARMA.
XX PI Romagne F, Andre P;
XX DR WPI; 2004-507595/48.
XX PT Pharmaceutical compositions that stimulate proliferation of natural
PT killer cells useful for therapy of melanoma, chronic myeloid, and
PT leukemia, comprise an anti-natural killer cell receptor antibody and
PT interleukins.
XX PS Claim 3; SEQ ID NO 2; 35pp; English.
XX CC The present sequence is that of the extracellular region of human Nkp30
CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by
CC natural killer (NK) cells, and particularly by mature NK cells. Claimed
CC pharmaceutical compositions that have a stimulating effect on the
CC proliferation of NK cells comprise an antibody such as an anti-Nkp30
CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
CC cytokine(s) and cytokine(s) being administered together or separately
CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its
CC antigen-binding fragment which specifically binds to Nkp30 or to a
CC fragment, including the extracellular region, of Nkp30. The
CC pharmaceutical compositions, when used for daily subcutaneous injection,
CC comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and
CC lower than 1 million units/square meters/day of cytokine(s), are useful
CC for the prevention, palliation and therapy of e.g. melanoma, chronic
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,
CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial
CC prevention, palliation and therapy (claimed).
XX SQ Sequence 120 AA;
XX MM 62.0%; Score 632; DB 8; Length 120;
XX Best Local Similarity 100.0%; Pred. No. 5,9e-54;
XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78
DB 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
QY 79 PLASSRFLHDHQAELHVRDVRGHDASTYVCRVEVLGVTGTGTRLVWEKEHPQLGAGT 138
DB 61 PLASSRFLHDHQAELHVRDVRGHDASTYVCRVEVLGVTGTGTRLVWEKEHPQLGAGT 120
RESULT 11
ADP48750
ID ADP48750 standard; protein; 382 AA.
XX AC ADP48750;
XX DT 09-SEP-2004 (first entry)
XX DE Human Nkp30-Fc conjugate protein SEQ ID NO:12.
XX KW polypeptide conjugate; target recognition; natural killer cell receptor;
KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;
KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;
KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;
KW human; natural killer cytotoxicity receptor conjugate;
KW Nkp30-Fc conjugate.
XX OS Homo sapiens.
XX FH Key
XX FT Peptide
XX FT Protein
XX FT /label= signal
XX FT 26..382
XX FT /note= "Nkp30-Fc conjugate"
XX FT Misc-difference 26..31
XX FT /note= "Kpni site"
XX FT Region 32..148
XX FT /label= Nkp30
XX FT Region 149..382
XX FT /label= Fc
XX PN WO2004053054-A2.
XX XX
XX PD 24-JUN-2004.
XX PF 09-DEC-2003; 2003WO-IL001040.
XX PR 09-DEC-2002; 2002US-0431728P.
XX PA (NATS-) NATSPEARS LTD.
XX PI Mandelboim O, Porgador A;
XX DR WPI; 2004-468830/44.
XX DR N-PSDB; ADP48757.
XX PT New polypeptide conjugate comprising a target recognition segment
XX comprising a Natural Killer cell receptor consisting of Nkp30, useful in
XX preparing a composition for treating a neoplastic disease.
XX PS Claim 5; SEQ ID NO 4; 66pp; English.
XX CC The present invention describes a polypeptide conjugate comprising: (a) a
XX target recognition segment comprising a natural killer cell receptor
XX (NCR) or its fragment consisting of Nkp30 or its fragment that binds to a
XX cellular ligand expressed on the surface of a target tumour cell; and (b)
XX a second segment comprising an active agent capable of exerting a
XX cytotoxic effect on the target cell. Also described: (1) an isolated
XX polynucleotide encoding the polypeptide conjugate; (2) a vector
XX comprising the polynucleotide; (3) a host cell comprising the vector and
XX capable of expressing the polypeptide conjugate; (4) a pharmaceutical
XX composition comprising the polypeptide conjugate and a carrier,
XX stabiliser or diluent; (5) treating a neoplastic disease in a subject;
XX (6) inhibiting the growth of a tumour in a subject; and (7) delivering a
XX cytotoxic substance to a target tumour cell in a subject. The polypeptide
XX conjugate has cytostatic activity, and can be used in gene therapy. The
XX polypeptide conjugate is useful in preparing a composition for treating a
XX neoplastic disease associated with a solid tumour or a non-solid tumour,
XX e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell
XX carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell
XX lymphoma or leukaemia. The present sequence represents a human natural
XX killer cytotoxicity receptor conjugate, designated Nkp30-Fc conjugate,
XX which is used in the exemplification of the present invention.
XX SQ Sequence 382 AA;
XX MM 59.7%; Score 608.5; DB 8; Length 382;
XX Best Local Similarity 85.8%; Pred. No. 5,3e-51;
XX Matches 121; Conservative 5; Mismatches 6; Indels 9; Gaps 2;
QY 1 MAWMLLLILIMVHPGSC-----ALWVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVT 54
DB 11 LATLVLLGLMLV---ASCLGRILRVPLWVSQPLEIRTLGSSAFPCSFNASQGRLAIGSVT 67
QY 55 WFRDEVVPGKEVRNGTPEFRGLAFLASSRFLHDHQAELHVRDVRGHDASTYVCRVEVLG 114
DB 68 WFRDEVVPGKEVRNGTPEFRGLAFLASSRFLHDHQAELHVRDVRGHDASTYVCRVEVLG 127
QY 115 LGVGTGTGTRLVWEKEHPQLG 135

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Db 128 LGVGTGNGTRLVWEKHPQLG 148

RESULT 12  
AAE02773  
ID AAE02773 standard; peptide; 33 AA.  
XX AC AAE02773;  
XX DT 06-AUG-2001 (first entry)  
XX DE Human Nkp30 receptor intracellular region sequence.  
XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
XX KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
XX KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
XX KW therapy; intracellular region.  
XX OS Homo sapiens.  
XX FN WO200136630-A2.  
XX PD 25-MAY-2001.  
XX PF 15-NOV-2000; 2000WO-EP011697.  
XX PR 15-NOV-1999; 99CA-02288307.  
XX PR 15-NOV-1999; 99US-00440514.  
XX PA (INNA-) INNATE PHARMA SAS.  
XX PA (UYGE-) UNIV GENOVA.  
XX PI Moretta A, Bottino C, Biassoni R;  
XX XX  
XX DR WPI; 2001-329221/34.  
XX XX Novel compound, useful for detection and/or quantifying the presence of  
XX FT NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
XX PS Claim 1; Fig 7B; 83pp; English.

XX CC The invention relates to human Nkp30 receptor and its corresponding cDNA  
XX CC molecule which is involved in natural cytotoxicity mediated by natural  
XX CC killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
XX CC is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
XX CC expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
XX CC useful for detecting and/or quantifying the presence of NK cells in a  
XX CC biological sample. The invention also provide kits for detecting and/or  
XX CC quantifying the presence of NK cells, for the selective removal of NK  
XX CC cells from a biological sample, for the positive and selective  
XX CC purification of NK cells from a biological sample and for the in vitro  
XX CC stimulation of NK cell cytotoxicity. The invention further provides a  
XX CC pharmaceutical composition which is used as a drug for grafting  
XX CC enhancement, graft versus host (GVH) inhibition, stimulation of graft  
XX CC versus tumour (Gvt) and especially graft versus leukaemia (GvL), and for  
XX CC the prevention, palliation and/or therapy of solid or liquid tumours,  
XX CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
XX CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
XX CC identifying Nkp30 natural ligands and allow assessment of the level of  
XX CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
XX CC comparison of this level to the standard physiological one. Hence Nkp30  
XX CC antibodies are useful in the diagnosis of tumours or of infection. The  
XX CC present sequence is the intracellular region of human Nkp30 receptor  
XX SQ Sequence 33 AA;

Query Match 20.0%; Score 204; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0;  
QY 158 STVYQKCHCHMGTHCHSSDGRGVPEPCP 190  
Db 1 STVYQKCHCHMGTHCHSSDGRGVPEPCP 33

RESULT 13  
ADO30926  
ID ADO30926 standard; protein; 33 AA.  
XX AC ADO30926;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human Nkp30 cytoplasmic tail.  
XX KW Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.  
XX OS Homo sapiens.  
XX PN WO2004056392-A1.  
XX PD 08-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-EP014716.  
XX PR 23-DEC-2002; 2002US-0435344P.  
XX PA (INNA-) INNATE PHARMA.  
XX PI Romagne F, Andre P;  
XX XX  
XX DR WPI; 2004-507595/48.

XX PT Pharmaceutical compositions that stimulate proliferation of natural  
XX PT killer cells useful for therapy of melanoma, chronic myeloid, and  
XX PT leukemia, comprise an anti-natural killer cell receptor antibody and  
XX PT interleukins.  
XX PS Claim 3; SEQ ID NO 4; 35pp; English.  
XX CC The present sequence is that of the cytoplasmic tail of human Nkp30  
XX CC ADO30926, a 190 amino acid polypeptide that is selectively expressed by  
XX CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
XX CC pharmaceutical compositions that have a stimulating effect on the  
XX CC proliferation of NK cells comprise an antibody such as an anti-Nkp30  
XX CC antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a  
XX CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
XX CC antibody(ies) and cytokine(s) being administered together or separately  
XX CC to a subject. The anti-Nkp30 antibody is an isolated antibody or its  
XX CC antigen-binding fragment which specifically binds to Nkp30 or to a  
XX CC fragment, including the cytoplasmic tail, of Nkp30. The pharmaceutical  
XX CC compositions, when used for daily subcutaneous injection, comprising from  
XX CC 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1  
XX CC million units/square meters/day of cytokine(s), are useful for the  
XX CC prevention, palliation and therapy of e.g. melanoma, chronic myeloid  
XX CC leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, and  
XX CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
XX CC prevention, palliation and therapy (claimed).

XX SQ Sequence 33 AA;  
Query Match 20.0%; Score 204; DB 8; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-12; Indels 0; Gaps 0;  
Matches 33; Conservative 0; Mismatches 0;  
QY 158 STVYQKCHCHMGTHCHSSDGRGVPEPCP 190  
Db 1 STVYQKCHCHMGTHCHSSDGRGVPEPCP 33

RESULT 14  
AAE02073  
ID AAE02073 standard; protein; 246 AA.  
XX AC AAE02073;  
XX XX

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DT 18-JUN-2002 (first entry)
XX Human lung specific gene (LSG) protein #11.
XX DE
XX Human; lung specific gene; LSG; lung embryonic development; cytostatic;
XX KW lung cancer; vaccine; gene therapy; non-cancerous lung disease; tumour.
XX KW
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX FH 189..204
XX FT Region
XX FT /note= "Antigenic epitope"
XX FT
XX PN WO200208278-A2.
XX XX
XX 31-JAN-2002.
XX PD
XX 20-JUL-2001; 2001WO-US022949.
XX PF
XX 21-JUL-2000; 2000US-0219834P.
XX PR
XX (DIAD-) DIADEXUS INC.
XX PA
XX Macina RA, Nair M, Chen S;
XX PI
XX WI; 2002-268964/31.
XX DR
XX Novel lung specific gene useful for identifying, diagnosing, monitoring,
XX PT staging, imaging and treating lung cancer and non-cancerous disease
XX PT states in lung, for gene therapy, and for identifying lung tissue.
XX PT
XX PS Claim 2; Page 178-179; 197pp; English.
XX XX
XX The present invention relates to lung specific genes (LSG) and their
XX CC corresponding polypeptides. LSG is useful for identifying, diagnosing,
XX CC monitoring, staging, imaging and treating lung cancer and non-cancerous
XX CC disease states in lung, identifying lung tissue, monitoring and modifying
XX CC lung embryonic development and differentiation, in gene therapy, as
XX CC hybridisation probes, to detect LSG mRNA as a marker for lung cancer, as
XX CC research reagents and materials for discovery of treatments and
XX CC diagnostics to human disease, to detect complementary polynucleotides,
XX CC and for chromosome identification. An antibody which binds LSG is useful
XX CC to detect or image localisation of LSG in a patient for detecting or
XX CC diagnosing a disease or condition, for preventing the onset and treatment
XX CC of lung cancer, to isolate or to identify clones expressing LSG
XX CC polypeptides, to purify LSG polypeptides, and to target tumours
XX CC expressing LSG. The present sequence is human LSG protein
XX XX
XX Sequence 246 AA;
XX SQ
Query Match 12.1%; Score 123.5; DB 5; Length 246;
Best Local Similarity 29.2%; Pred. No. 0.0013;
Matches 54; Conservative 17; Mismatches 61; Indels 53; Gaps 10;

QY 1 MAWM-LLLLIMVHPGSCALWV-SQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFWRD 58
DB 1 MAWAPLLTLLSLTGSILQSPILQTPPSASASLGASVTLTCSVSSDYKNL---EVDWFOQ 57
QY 59 EWPVQKEVR-----NGTPEFRGLAP-----LASSRFLDHQAEHLHVRGHDAS 104
DB 58 R--FGKGRFVMRYGTGVGFCRADIPDRFSVSGSLNRF-----LIRNIEEDES 108
QY 105 IYVCRVEVLGUGVT-----GNGTRLV-----EKEHPQLGAGTVLL 142
DB 109 DYHCGTD---LGSCTSFVSWVFGGGLTTLVLSQPKAAPSVTLPPPSSEELQANKATLVCL 165
QY 143 RAGFY 147
DB 166 ISDFY 170

18-JUN-2002 standard; protein; 232 AA.
ABU08020;
ABU08020;
10-MAY-2003 (first entry)
Monoclonal rabies virus antibody light chain, clone JB.1.
Human; antibody; constant region; monoclonal antibody 57; Mab 57;
variable region; Rabies; neurological disease; infection;
central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
pathogen; vaccine; virucide; light chain.
Homo sapiens.
WO2003016501-A2.
27-FEB-2003.
21-AUG-2002; 2002WO-US026584.
21-AUG-2001; 2001US-0314023P.
(UYOE-) UNIV JEFFERSON THOMAS.
Hooper DC, Dietzschold B;
WPI; 2003-278566/27.
N-PSDB; ABX12862.
New recombinant antibody comprising a constant region of Mab 57 linked to
a non-Mab 57 variable region, useful for treating an individual exposed
to a pathogen, e.g. rabies infection.
Claim 1; Page 36; 38pp; English.
The invention discloses a recombinant antibody comprising a constant
region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
region. Rabies is an acute, neurological disease caused by infection of
the central nervous system with the rabies virus, a member of the
Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
for producing an isolated recombinant antibody by culturing a host cell,
for producing a recombinant expression vector comprising the nucleic acid
molecule encoding the antibody, and isolating the recombinant antibody
expressed and treating an individual exposed to a pathogen by
administering to the individual the recombinant antibody. The recombinant
antibodies are useful for preventing (vaccine) and treating an individual
exposed to a pathogen, e.g. rabies infection. They are also useful for
the qualitative and quantitative determination of the rabies virus. The
sequences presented are the antibody protein fragments, the nucleic acids
encoding them or the PCR primers used to construct the recombinant
expression vector
Sequence 232 AA;
Query Match 11.7%; Score 119.5; DB 6; Length 232;
Best Local Similarity 26.0%; Pred. No. 0.0029;
Matches 45; Conservative 25; Mismatches 64; Indels 39; Gaps 7;

QY 1 MAWMLLLILIMVH-PCSCALWV-SQPPEIRTLGSSAFPCSFNASQGRLAIGSVTFWRD 58
DB 1 MAWTVLLGLLSHCTGTSVTSVLTQTPSVSVAPGKTARINCGNNIEYR---SVHWYQQ 56
QY 59 E-----VVPQKEVRNGTPE-FRGLAPLASSRFLDHQAEHLHVRGHDASIVYCR 109
DB 57 KSGQAPVAVIYDNSDRPSGIPERFSGSKS-----GNTATLTISRVEAGDEADYVCO 107
QY 110 VEVLGLGVTGNGTRLV-----EKEHPQLGAGTVLLRAGFY 147
DB 108 VWDISSDVVFGGGLTTLVLSQPKAAPSVTLPPPSSEELQANKATLVCLISDFY 160

Search completed: November 16, 2004, 18:55:51

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Wed Nov 17 05:46:29 2004

us-10-036-444-2.open.rag

Page 10

Job time : 206.095 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 169.841 Seconds  
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395.915 Million cell updates/sec

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Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pap.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pap.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pap.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pap.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pap.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pap.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pap.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pap.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pap.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pap.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pap.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pap.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pap.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pap.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	100.0	190	13	US-10-036-444-2
2	1020	100.0	190	16	US-10-696-259-4
3	956.5	93.8	185	16	US-10-696-259-7
4	876	85.9	201	16	US-10-696-259-6
5	859	84.2	177	16	US-10-696-259-5
6	842.5	82.6	198	16	US-10-696-259-9
7	828.5	81.2	161	16	US-10-696-259-10
8	825	80.9	175	16	US-10-696-259-8
9	713	69.9	135	15	US-10-333-481-17
10	713	69.9	369	15	US-10-333-481-18
11	632	62.0	120	13	US-10-036-444-4
12	204	20.0	33	13	US-10-036-444-6
13	123.5	12.1	246	10	US-09-909-567B-49

14	119.5	11.7	232	14	US-10-225-108A-12	Sequence 12, Appli
15	119.5	11.7	232	15	US-10-461-148-6	Sequence 6, Appli
16	118.5	11.6	139	14	US-10-312-495-6	Sequence 6, Appli
17	118.5	11.6	212	10	US-09-898-195A-17	Sequence 17, Appli
18	118.5	11.6	212	14	US-10-057-288-12	Sequence 12, Appli
19	118.5	11.6	212	14	US-10-155-514-2	Sequence 2, Appli
20	118.5	11.6	212	15	US-10-419-008-17	Sequence 17, Appli
21	111.5	10.9	226	13	US-10-038-107A-1	Sequence 1, Appli
22	111.5	10.9	226	14	US-10-371-525-32	Sequence 32, Appli
23	111.5	10.9	226	14	US-10-371-069-32	Sequence 32, Appli
24	111.5	10.9	226	14	US-10-371-645-32	Sequence 32, Appli
25	111.5	10.9	226	14	US-10-371-260-32	Sequence 32, Appli
26	111.5	10.9	226	14	US-10-411-010-19	Sequence 19, Appli
27	111	10.9	223	15	US-10-383-201-20	Sequence 20, Appli
28	110	10.8	223	9	US-09-989-545-21	Sequence 21, Appli
29	110	10.8	223	10	US-09-928-267-18	Sequence 18, Appli
30	110	10.8	223	10	US-09-928-267-21	Sequence 21, Appli
31	110	10.8	223	14	US-10-225-519-8	Sequence 8, Appli
32	110	10.8	223	14	US-10-207-655-101	Sequence 101, App
33	108.5	10.6	223	9	US-09-989-545-20	Sequence 20, Appli
34	108.5	10.6	223	14	US-10-211-207-5	Sequence 5, Appli
35	108.5	10.6	223	14	US-10-077-106-5	Sequence 5, Appli
36	108.5	10.6	223	16	US-10-750-396-42	Sequence 42, Appli
37	108.5	10.6	223	17	US-10-748-112-19	Sequence 11, Appli
38	108.5	10.6	383	10	US-09-898-195A-11	Sequence 11, Appli
39	108.5	10.6	383	14	US-10-057-288-6	Sequence 6, Appli
40	108.5	10.6	383	14	US-10-155-514-10	Sequence 10, Appli
41	108.5	10.6	383	15	US-10-419-008-11	Sequence 11, Appli
42	108	10.6	223	13	US-10-107-828-26	Sequence 26, Appli
43	108	10.6	223	13	US-10-107-907-26	Sequence 26, Appli
44	108	10.6	223	13	US-10-107-868-26	Sequence 26, Appli
45	108	10.6	223	14	US-10-301-056-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1  
US-10-036-444-2  
; Sequence 2, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNAVE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "NO. US20020142445alel triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 190  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-2

Query Match 100.0%; Score 1020; DB 13; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3.1e-93; Mismatches 0; Indels 0; Gaps 0;  
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAWMLLLILIMVHPSGSCALWVSQPPPIRTLEGSSAFPCSFNASCRLAIGSVTFRDEV 60  
Sequence 10, Appli  
Db 1 MAWMLLLILIMVHPSGSCALWVSQPPPIRTLEGSSAFPCSFNASCRLAIGSVTFRDEV 60  
Sequence 17, Appli  
QY 61 VPGKEVRNGTPEFRGLADPLASSRLHLDHQAELHIRDVRGHDAIYVCEVVLGLGVGTG 120  
Sequence 4, Appli  
Db 61 VPGKEVRNGTPEFRGLADPLASSRLHLDHQAELHIRDVRGHDAIYVCEVVLGLGVGTG 120  
Sequence 49, Appli

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QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
QY 181 RGVIPERPCP 190
DB 181 RGVIPERPCP 190

RESULT 2
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BROWNING, Jeffrey
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4
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Best Local Similarity 100.0%; Pred. No. 3.1e-93;
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DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
QY 181 RGVIPERPCP 190
DB 181 RGVIPERPCP 190

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US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: BROWNING, Jeffrey
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; PRIOR FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7
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Best Local Similarity 89.2%; Pred. No. 7.2e-79;
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QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
DB 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
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; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7
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Best Local Similarity 96.8%; Pred. No. 6.3e-87;
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DB 1 MAWMLLLILIMVHPGSCALWVSQPPETRTLGSSAFPLPCSFNASQGRLAIGSVTWFRDEV 59
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DB 60 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 118
QY 121 NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFSLVAVGSTVYYQKCHCHMGTHCHSSDGP 180
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QY 181 RGVIPERPCP 190
DB 177 -GVIPERPCP 185

RESULT 4
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6
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Best Local Similarity 89.2%; Pred. No. 7.2e-79;
Matches 173; Conservative 2; Mismatches 7; Indels 12; Gaps 2;
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QY 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
DB 61 VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTG 120
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RESULT 5
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; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      84.2%; Score 859; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 3e-77;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
QY      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQK 165
Db      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQK 165

RESULT 6
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
US-10-696-259-9

Query Match      81.2%; Score 828.5; DB 16; Length 161;
Best Local Similarity 99.4%; Pred. No. 2.9e-74;
Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 119
QY      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYY 162
Db      120  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYY 161

RESULT 8
US-10-696-259-8
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; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match      82.6%; Score 842.5; DB 16; Length 198;
Best Local Similarity 88.1%; Pred. No. 1.5e-75;
Matches 170; Conservative 2; Mismatches 8; Indels 13; Gaps 4;

QY      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 59
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db      60  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 118
QY      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYQKCHMGTCHSSDGP 180
Db      119  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYYHGK-----CLTWKGP 170
QY      181  R---GVIPERCP 190
Db      171  RRLFAVVPAPLPP 183

RESULT 7
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-10

Query Match      81.2%; Score 828.5; DB 16; Length 161;
Best Local Similarity 99.4%; Pred. No. 2.9e-74;
Matches 161; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
Db      1  MAWMLLLILIMVHPGSCALWVSQPPEIRTLGGSSAFLPCSFNASQGRLAIGSVTWERDEV 60
QY      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 120
Db      61  VPGKEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLGVGTG 119
QY      121  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYY 162
Db      120  NGTRLVVEKEHPQLGAGTVLLLRAGFYAVSFLSVAVGSTVYY 161

RESULT 8
US-10-696-259-8
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; Sequence 8, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR FILING DATE: 2003-10-28  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-696-259-8

Query Match 80.9%; Score 825; DB 16; Length 175;  
Best Local Similarity 98.2%; Pred. No. 7.2e-74;  
Matches 162; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPETRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEV 59  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
DB 60 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 118  
QY 121 NGTRLVVKEHPQLGAGTLLLRAGFVAVSFLSVAGSVTVYCGK 165  
DB 119 NGTRLVVKEHPQLGAGTLLLRAGFVAVSFLSVAGSVTVYHGK 163

RESULT 9  
US-10-333-481-17  
; Sequence 17, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Ofer Mandelboim  
; APPLICANT: Angel Porcador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSIS  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; PRIOR FILING DATE: 2003-08-04  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-17

Query Match 69.9%; Score 713; DB 15; Length 135;  
Best Local Similarity 100.0%; Pred. No. 7.3e-63;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120

Db 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
QY 121 NGTRLVVKEHPQLG 135  
DB 121 NGTRLVVKEHPQLG 135

RESULT 10  
US-10-333-481-18  
; Sequence 18, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Ofer Mandelboim  
; APPLICANT: Angel Porcador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSIS  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; PRIOR FILING DATE: 2003-08-04  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-18

Query Match 69.9%; Score 713; DB 15; Length 369;  
Best Local Similarity 100.0%; Pred. No. 2.6e-82;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
DB 1 MAMLLILIMVHPGSCALWVSQPPETRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEV 60  
QY 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
DB 61 VPGKEVNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTG 120  
QY 121 NGTRLVVKEHPQLG 135  
DB 121 NGTRLVVKEHPQLG 135

RESULT 11  
US-10-036-444-4  
; Sequence 4, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-PR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-4

Query Match 62.0%; Score 632; DB 13; Length 120;  
Best Local Similarity 100.0%; Pred. No. 7.3e-55;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

	LWVSPPPIRLTESSAFLPCSFNASQRIAGISVTFWRDEVVPVGKEVRNTPFEGR	78
Qy		
	1 LWVSPPPIRLTESSAFLPCSFNASQRIAGISVTFWRDEVVPVGKEVRNTPFEGR	60
Db		
	79 PLASRRFLDHQAELHLDVRGHDASIVYCRVEVLGVGTGNTRLVWEKHPQLG	138
Qy		
	61 PLASRRFLDHQAELHLDVRGHDASIVYCRVEVLGVGTGNTRLVWEKHPQLG	120
Db		

RESULT 12  
US-10-036-444-6  
; Sequence 6, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "NO. US202020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-PR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-6

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RESULT 13
US-09-909-567B-49
; Sequence 49, Application US/09909567B
; Publication No. US20030022257A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto A.
; APPLICANT: Nair, Manoj
; APPLICANT: Chen, Saiyi
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
; FILE REFERENCE: DEX-0214
; CURRENT APPLICATION NUMBER: US/09/909,567B
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,834
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 246
; TYPE: EXT
; ORGANISM: Homo sapien
US-09-909-567B-49
Query Match 12.1%; Score 123.5; DB 10; Length 246;
Best Local Similarity 29.2%; Pred. No. 0.00073;
Matches 54; Conservative 17; Mismatches 61; Indels 53; Gaps 10;
Qy 1 MAWV-LLILINVHPGSCALWV-QOPPEIRLTGSSAFLPCSFNASQGRLAIGSVTWPRD 58
Db 1 MAWAPLLILTLGLSLTGSLOPILTOPPSASASLGCASVLTLCVSVDYKYL---EVDWFOQ 57

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Qy	59	EVVPGKEVR-----NGTPEERGLAP-----LASSRFLDHQAEHLIRVVRGHDA	104
Db	58	R--PGKPGFVNRVGTGVVGFAGDIPDEFVSVSGCLNRF-----LTIRNIEEDES	108
Qy	105	IYVCRVEVLGLVGT-----GNCTRLLV-----EKEHQLGAGTVLL	142
Db	109	DHCGGD---LGSGTSEVSVVFGGGTKLTVLSQPKAAPSVTLPFPSEELQANKATLVCL	165
Qy	143	RAGFY	147
Db	166	ISDFY	170

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RESULT 14
US-10-225-108A-12
; Sequence 12, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225,108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-12

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RESULT 15  
US-10-461-148-6  
; Sequence 6, Application US/10461148  
; Publication No. US20040013672A1  
; GENERAL INFORMATION:  
; APPLICANT: Dietzschold, Bernhard  
; APPLICANT: Hooper, Douglas C.  
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS  
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME  
; FILE REFERENCE: 8321-110CII-185685  
; CURRENT APPLICATION NUMBER: US/10/461,148  
; CURRENT FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 10/225,108  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/314,023  
; PRIOR FILING DATE: 2001-08-21



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 53.4218 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-2  
Perfect score: 1020  
Sequence: 1 MAWMLLLILIMVHPSGALW.....GTHCHSSDGRGVIEPRCP 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A COMB.pcp.\*  
2: /cgn2\_6/prodata/1/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/1/iaa/6A COMB.pcp.\*  
4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/PCUTS COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	112	11.0	223	3	US-08-228-208A-17
2	111.5	10.9	226	4	US-09-311-784A-32
3	106.5	10.4	364	4	US-09-472-087-100
4	106	10.4	270	3	US-09-082-593-10
5	104.5	10.2	238	4	US-09-227-595-30
6	104.5	10.2	238	4	US-09-227-595-32
7	104.5	10.2	238	4	US-08-595-590B-30
8	104.5	10.2	238	4	US-08-595-590B-32
9	104	10.2	174	3	US-08-804-180C-4
10	103.5	10.1	187	1	US-08-067-684-14
11	103.5	10.1	187	1	US-08-068-898-14
12	103.5	10.1	187	2	US-08-459-818-14
13	103.5	10.1	187	2	US-08-889-666-14
14	103.5	10.1	187	2	US-08-465-078-14
15	103.5	10.1	187	2	US-08-725-776-14
16	103.5	10.1	187	2	US-08-488-062-14
17	103.5	10.1	187	3	US-08-228-208A-14
18	103.5	10.1	187	4	US-08-223-783-36
19	103.5	10.1	187	5	PCT-US95-06726-36
20	103.5	10.1	236	3	US-09-049-672A-7
21	103	10.1	267	1	US-08-416-336-2
22	102.5	10.0	223	4	US-09-303-040-10
23	101.5	10.0	374	4	US-09-227-595-26
24	101.5	10.0	374	4	US-09-227-595-28
25	101.5	10.0	374	4	US-08-595-590B-26
26	101.5	10.0	374	4	US-08-595-590B-28
27	101.5	10.0	377	4	US-09-227-595-24

Sequence 24, Appl  
Sequence 26, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 19, Appl  
Sequence 1, Appl  
Sequence 2, Appl

28 101.5 10.0 377 4 US-08-595-590B-24  
29 100 9.8 239 4 US-09-828-995B-26  
30 98.5 9.7 526 4 US-09-910-174B-9  
31 98.5 9.7 526 4 US-09-820-461-9  
32 98 9.6 589 2 US-08-724-394A-1  
33 97 9.5 131 1 US-08-305-683A-4  
34 97 9.5 253 2 US-08-459-818-20  
35 97 9.5 253 2 US-08-889-666-20  
36 97 9.5 253 2 US-08-465-078-20  
37 97 9.5 253 2 US-08-725-776-20  
38 97 9.5 253 2 US-08-488-062-20  
39 97 9.5 502 2 US-08-459-818-19  
40 97 9.5 502 2 US-08-889-666-19  
41 97 9.5 502 2 US-08-465-078-19  
42 97 9.5 502 2 US-08-725-776-19  
43 97 9.5 502 2 US-08-488-062-19  
44 95.5 9.4 218 4 US-10-026-045-1  
45 95.5 9.4 218 4 US-10-026-045-2

ALIGNMENTS

RESULT 1  
US-08-228-208A-17  
; Sequence 17, Application US/08228208A  
; Patent No. 6090914  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Dams, Nitin K.  
; APPLICANT: Brady, William  
; APPLICANT: Wallace, Philip M.  
; TITLE OF INVENTION: CTLA4/CD28lg HYBRID FUSION  
; TITLE OF INVENTION: PROTEINS AND USES THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 1150 Santa Monica Boulevard, Suite 400  
; CITY: Los Angeles  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 90025

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/228,208A  
FILING DATE: 15-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/008,898  
FILING DATE: 22-JAN-1993  
APPLICATION NUMBER: 07/723,617  
FILING DATE: 27-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Adriano, Sarah B  
REGISTRATION NUMBER: 34,470  
REFERENCE/DOCKET NUMBER: 30436-30US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 310 445-1140  
TELEFAX: 310 445-9031  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-228-208A-17

Query Match 11.0%; Score 112; DB 3; Length 223;  
Best Local Similarity 28.0%; Pred. No. 0.00059;  
Matches 47; Conservative 22; Mismatches 75; Indels 24; Gaps 6;  
QY 6 LLLIMVHVGSC-ALWYSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFRDEVPGK 64  
DB 24 LFFELLIPVCKAMHVAQPAVLAASSRGIAFVCEY-ASPGKATEVRVTVLQADSQVT 82  
QY 65 EVRNGTPEFRGLAPLASSRFLHD-----HQAEHLHIRDVGHDAIYVCRVRL-- 113  
DB 83 EVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYP 136  
QY 114 -GLGVGTGNGTRLVVEKEHPQLGAGTVLLLR-----CFYAVSFLSVAV 156  
DB 137 PPYLIGNGTQIYVIDPECPDSDFLMLTAAVSSGLFFYSFLLTAV 184  
RESULT 2  
US-09-311-784A-32  
; Sequence 32, Application US/09311784A  
; Patent No. 6534462  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human MB-1 Ig-alpha  
US-09-311-784A-32

Query Match 10.9%; Score 111.5; DB 4; Length 226;  
Best Local Similarity 28.0%; Pred. No. 0.00067;  
Matches 47; Conservative 24; Mismatches 70; Indels 27; Gaps 8;  
QY 4 MLLILIMVHVGSCALWVSQ-PEIRTLGSSAFPLPCSFNASQGLAIGSVTWFRDEVVP 62  
DB 18 LFLLSAVYLGPGCQALMHEKVPASLMSVLGSDAHFQCPHNSNN---ANVTWWR--VLH 71  
QY 63 GKEVRNGT--PEFRGLAPLASSRFLHDQAEHLHIRDVGHDAIYVCRVRLGCVGTG 120  
DB 72 G-----NYTWPPFLGP-----CEDPNGTLLIQNVKSHGGIYVCRVQEGNESYQOS 118  
QY 121 NGTRLVVEKEHPQ-----LGAGTV-LLLRAGFYAVSFLSVAVGSTVYVQ 163  
DB 119 CGTYLAVRQPPPPFPFLDMGEGTKNRIITAEGIILLFCAVVPGLTLFR 166

RESULT 3  
US-09-472-087-100  
; Sequence 100, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, EILEEN E.  
; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR FILING DATE: 60/113,647  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 364  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; ORGANISM: Homo sapiens  
US-09-472-087-100

Query Match 10.4%; Score 106.5; DB 4; Length 364;  
Best Local Similarity 28.0%; Pred. No. 0.0044;  
Matches 40; Conservative 20; Mismatches 62; Indels 21; Gaps 5;  
QY 4 MLLILIMVHVP--GSCALWVSQPPEIRTLGSSAFPLPCSFNASQGLAIGSVTWFRDEVV 61  
DB 10 LLSLVALLFPMSMASMAHVAQPAVLAASSRGIAFVCEY-ASPGKATEVRVTVLQADS 68  
QY 62 PGKEVRNGTPEFRGLAPLASSRFLHD-----HQAEHLHIRDVGHDAIYVCRVVEV 112  
DB 69 QVTEVCAATYMMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL 122  
QY 113 L---GLGVGTGNGTRLVVEKEHP 132  
DB 123 MYPPPYLIGNGTQIYVIDPEP 145

RESULT 4  
US-09-082-593-10  
; Sequence 10, Application US/09082593  
; Patent No. 6180104  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, MARK M.  
; APPLICANT: HEDRICK, STEPHEN M.  
; TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT  
; FILE REFERENCE: JX1193-195DIV2  
; CURRENT APPLICATION NUMBER: US/09/082,593  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-082-593-10

Query Match 10.4%; Score 106; DB 3; Length 270;  
Best Local Similarity 25.8%; Pred. No. 0.0033;  
Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;  
QY 3 WMLLLILIMVHVGSCALWVS-----QPPEIRTLGSSAFPLPCSFNASQGLAIGSVTW 55  
DB 12 WLLL-----NWVNSQNVQVQSPESLIVPEGARTSLNCTSDSASQY-----FWW 55  
QY 56 FREVVPKKEVR-----NGTEPFRGLAPLASSRFLHDQAEHLHIRDVGHDAIYVVC 108  
DB 56 YROH--SGKAPKALMIFNGEXE-EGRTTIHINKASLH---FSLHIRDSQPSDSALYLC 109  
QY 109 RVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLR 143  
DB 110 AVTLYG-----GSGNKLI-----FGTGLLSVK 132

RESULT 5  
US-09-227-595-30  
; Sequence 30, Application US/09227595

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; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/595,590
; FILING DATE: February 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-227-595-30

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTW 55
Db 1 MGWSCIIILFVATATGVH---SAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGRPLAFLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPPIYLGIGNGAQITVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFY 164

RESULT 6
US-09-227-595-32
; Sequence 32, Application US/09227595
; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

; Patent No. 6444792
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; TITLE OF INVENTION: Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/595,590
; FILING DATE: February 2, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-09-227-595-32

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSOPPEIRTLGSSAFPLPCSFNASQGRLAIGSVTW 55
Db 1 MGWSCIIILFVATATGVH---SAMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGRPLAFLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTGNGTRLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPPIYLGIGNGAQITVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFY 164

RESULT 7
US-08-595-590B-30
; Sequence 30, Application US/08595590B
; Patent No. 6750334
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; Having Modified Effector Functions and Uses Therefor
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-08-595-590B-30

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVWLASSRGIAFVCEY-ASEGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTNGTGLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFPPSDEQLKSGTASVVCCLNNFY 164

RESULT 8
US-08-595-590B-32
; Sequence 32, Application US/08595590B
; Patent No. 6750334
; GENERAL INFORMATION:
; APPLICANT: Gray, Gary S. et al.
; TITLE OF INVENTION: CTLA4-Immunoglobulin Fusion Proteins
; Having Modified Effector Functions and Uses
; Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-Windows
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,590B
; FILING DATE: 02-Feb-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; NAME: Amy E. Mandragoras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-007CPA2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-595-590B-32
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 238 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-595-590B-32

Query Match 10.2%; Score 104.5; DB 4; Length 238;
Best Local Similarity 24.7%; Pred. No. 0.0041;
Matches 43; Conservative 24; Mismatches 70; Indels 37; Gaps 7;

QY 1 MAWMLLLILIM-----VHPGSCALWVSOPPEIRTLGSSAFPLCSFNASQRLAIGSVTW 55
Db 1 MGWSCIILFLVATATGVH---SAMHVAQPAVWLASSRGIAFVCEY-ASEGKATEVRVTV 56
QY 56 FRDEVVPGKEVRNGTPEFRGLAPLASSRFLHD-----HQAELHIRDVRGHDASIY 106
Db 57 LRQADSQVTEVCAATYMMGNELT-----FLDSDICTGTSSGNQVNLTIQGLRAMDTGLY 110
QY 107 VCRVEVL---GLGVGTNGTGLV-----EKEHPQLGAGTVLLLRAGFY 147
Db 111 ICKVELMYPYPYILGIGNGAQITVAAPSVFIFPPSDEQLKSGTASVVCCLNNFY 164

RESULT 9
US-08-804-180C-4
; Sequence 4, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
; DESCRIPTION: no
; HYPOTHETICAL: no
; FRAGMENT TYPE: Internal fragment
; ORIGINAL SOURCE:
; ORGANISM: Rattus No. 6107056vegicus
; STRAIN: ACI
; DEVELOPMENTAL STAGE: Adult
; CELL TYPE: Splenocyte
; FEATURE:
; NAME/KEY: Rat sCTLA-4
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; Sequence 14, Application US/08459818
; Patent No. 5851795
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,818
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436.35US02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-818-14

Query Match      10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPPETRLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDSDICTGSSGNQNLTIQGRAMDTGLYICKVELMYPYPYLGIGNGTOI 113

QY 126 VVEKEHPQLGAGTVLLRA----GFYAVSFLSVAV 156
Db 114 YVIDPECPDSDFLWILAAVSSGLFPYSFLLTAV 148

RESULT 13
US-08-889-666-14
; Sequence 14, Application US/08898666
; Patent No. 5885579
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles

```

```

; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/889,666
; FILING DATE: 08-JUL-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-889-666-14

Query Match      10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPPETRLGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMMGNEL 59

QY 78 APLASSRFLHD-----HQAELHIRDVRGHDASIVYCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDSDICTGSSGNQNLTIQGRAMDTGLYICKVELMYPYPYLGIGNGTOI 113

QY 126 VVEKEHPQLGAGTVLLRA----GFYAVSFLSVAV 156
Db 114 YVIDPECPDSDFLWILAAVSSGLFPYSFLLTAV 148

RESULT 14
US-08-465-078-14
; Sequence 14, Application US/08465078
; Patent No. 5885796
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damle, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/465,078
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 310-445-1140
; TELEFAX: 310-445-9031
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-078-14

Query Match          10.1%; Score 103.5; DB 2; Length 187;
Best Local Similarity 27.7%; Pred. No. 0.0038;
Matches 43; Conservative 20; Mismatches 69; Indels 23; Gaps 5;

QY 18 ALWVSQPEIRITLEGSSAFPCSNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGRL 77
Db 1 AMHVAQPAVVLASSRGIASFVCEY-ASPGKATEVRVTVLRLQADSQVTEVCAATYMGNEL 59
QY 78 APLASSRFLHD-----HQAEHLHTRDVRGHDSIYVCRVEVL---GLGVGTGNGTRL 125
Db 60 T-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYVLGIGNGTQI 113
QY 126 VVEKEHPQLGAGTVLLRA---GFYAVSFLSVAV 156
Db 114 YVIDPEPCDSDFLWLILAAVSSGLFFYSFLTLAV 148

Search completed: November 16, 2004, 19:17:42
Job time : 54.4218 secs
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RESULT 15
US-08-725-776-14
; Sequence 14, Application US/08725776
; Patent No. 5968510
; GENERAL INFORMATION:
; APPLICANT: Linsley, Peter S.
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Damie, Nitin K.
; APPLICANT: Brady, William
; APPLICANT: Kiener, Peter A.
; TITLE OF INVENTION: C11A4 Receptor and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 11150 Santa Monica Blvd., Suite 400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,776
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375390
; FILING DATE: 18-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Adriano, Sarah B.
; REGISTRATION NUMBER: 34,470
; REFERENCE/DOCKET NUMBER: 30436-35US01
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 24.8276 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-4  
Perfect score: 632  
Sequence: 1 LWVSQPPEIRTLGGSAFLP.....TGNGTLLVVEKHPQLGAGT 120  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: Piri:.\*  
2: Pir2:.\*  
3: Pir3:.\*  
4: Pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	116	18.4	132	2 A24402	T-cell receptor al
2	114.5	18.1	136	2 B45893	T-cell receptor al
3	107.5	17.0	138	2 C27577	T-cell receptor al
4	105	16.6	131	2 F45893	T-cell receptor al
5	103	16.3	129	2 A42692	T-cell receptor al
6	102.5	16.2	110	2 B24092	T-cell receptor al
7	101	16.0	120	2 I54487	T-cell receptor al
8	99.5	15.7	131	2 D24092	T-cell receptor al
9	99.5	15.7	131	2 E24092	T-cell receptor al
10	99	15.7	132	1 RWSAV	T-cell receptor al
11	98.5	15.6	130	2 A31211	T-cell receptor al
12	98.5	15.6	146	2 S26408	T-cell receptor al
13	97	15.3	139	2 S36325	T-cell receptor al
14	95.5	15.1	218	2 B47712	myelin/oligodendro
15	95.5	15.1	271	2 A53268	T-cell receptor al
16	94	14.9	526	2 S70587	butyrophilin precu
17	93.5	14.8	247	2 A5717	myelin/oligodendro
18	93	14.7	110	2 A24092	T-cell receptor al
19	93	14.7	117	2 I68824	T-cell receptor al
20	93	14.7	1694	2 S50065	sialoadhesin - mou
21	92.5	14.6	132	2 D45893	T-cell receptor al
22	92.5	14.6	139	2 S36302	T-cell receptor al
23	92.5	14.6	267	1 RWSCH	T-cell receptor al
24	91.5	14.5	107	2 S60590	IG heavy chain var
25	90	14.2	132	2 A27632	T-cell receptor al
26	89	14.1	134	2 A45893	T-cell receptor al
27	88.5	14.0	137	2 C45893	T-cell receptor al
28	88.5	14.0	223	2 A29063	cytotoxic T-lympho
29	88.5	14.0	264	2 F27579	T-cell receptor al

30	88.5	14.0	1197	2 T30581	neural cell adhesi
31	88	13.9	131	2 D44402	T-cell receptor al
32	88	13.9	226	2 A46477	membrane-bound imm
33	88	13.9	946	1 A47299	ror-related recept
34	87.5	13.8	111	2 JH0333	T-cell receptor al
35	87.5	13.8	132	2 S23374	T-cell receptor al
36	87.5	13.8	246	2 A47712	myelin/oligodendro
37	87.5	13.8	247	2 S58394	myelin/oligodendro
38	87	13.8	108	2 JH0342	T-cell receptor al
39	86.5	13.7	95	2 S0603	T-cell receptor al
40	86.5	13.7	129	2 S03478	T-cell receptor al
41	86.5	13.7	874	2 T29548	hypothetical prote
42	86.5	13.7	1273	2 T42405	sax-3 protein - Ca
43	86	13.6	140	2 PH0134	IG lambda chain pr
44	85.5	13.5	134	2 C29774	T-cell receptor al
45	85.5	13.5	223	2 T09536	cytotoxic T-lympho

ALIGNMENTS

RESULT 1  
A24402  
T-cell receptor alpha chain precursor V region (CS) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997  
C:Accession: A24402  
R:Becker, D.M.; Patten, P.; Chien, Y.; Yokota, T.; Eshhar, Z.; Giedlin, M.; Gascoigne, Nature 317, 430-434, 1995  
A:Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.  
A:Reference number: A93368; MUID:86014379; PMID:2995827  
A:Accession: A24402  
A:Molecule type: mRNA  
A:Residues: 1-132 <BEC>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 18.4%; Score 116; DB 2; Length 132;  
Best Local Similarity 33.3%; Pred.No. 0.00021;  
Matches 41; Conservative 16; Mismatches 42; Indels 24; Gaps 8;

QY 3 VSQPE--IRTLEGGSAFLPCSFNASQGRLAGISVTVWERDEWVPCKEV-----NGTPE 54  
DB 23 VQQPESLIIVEGAWVSLNCSFSDS-----ASQSIWVYQQH--PGKGRALISIFSGNKK 76  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLVGT---GNGTRLVVEK 111  
DB 77 -EGRLTVYLNRAHLH---VSLHIKDSQPSDAVYLCAVRSGANTGKLTGEGHTILAV-- 130  
QY 112 EHP 114  
DB 131 -HP 132

RESULT 2  
B45893  
T-cell receptor alpha chain precursor V region (BTA29) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: B45893  
R:Ishiguro, N.; Tanaka, A.; Shinagawa, M. Immunogenetics 31, 57-60, 1990  
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A:Reference number: A45893; MUID:90129157; PMID:2137108  
A:Accession: B45893  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <ISH>  
A:Cross-references: GB:P90011; NID:G217610; PIDN:BA014061.1; PID:G217611  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 18.1%; Score 114.5; DB 2; Length 136;

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Best Local Similarity 29.5%; Pred. No. 0.0003;
Matches 36; Conservative 18; Mismatches 39; Indels 29; Gaps 7;

QY 4 SQPEIRTEGSSAFPCSFNASQGRLAIGSVTFRDEVPVGVKVRNGTPEP-----55
Db 27 AEPASLPVEGAASLGCTYSNSLY-----FTWYRQ--YPKK-----GPEFLLOYANN 75

QY 56 ---RGR LAPASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGT-----GNGTRLV 109
Db 76 NKEBGRFT--AQSNKTKH--VSLIRDSBPSDSATYLCVCAVDTISTAGTKLTFGEGTRLI 132

QY 109 VE 110
Db 133 VK 134

RESULT 3
T-cell receptor alpha chain V region (5/10-20D) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C:Accession: C27577; C27557
R;Iwamoto, A.; Ohashi, P.S.; Pritchard, H.; Walker, C.B.; Michalopoulos, E.E.; Rupp, F.; H.
J. Exp. Med. 165, 591-600, 1987
A:Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. P
A:Reference number: A27557; MUID:87139812; PMID:3493320
A:Accession: C27577
A:Molecule type: mRNA
A:Residues: 1-138 <IWA>
A:Accession: C27557
A:Molecule type: mRNA
A:Residues: 22-138 <IW2>
A:Cross-references: EMBL:X05733
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 17.0%; Score 107.5; DB 2; Length 138;
Best Local Similarity 31.9%; Pred. No. 0.0015;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 3 VSQPEIRTEGSSAFPCSFNASQGRLAIGSVTFRDEVPVGVKVR-----NGTPE 54
Db 24 VQSPESLIVPEGAMTSLNCTFSDASQY-----FAWYRQ--SGKAPKALMIFNGEK 77

QY 55 FRGLAPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGTGNGTRLVVEKE 112
Db 78 -EGRFTHLNKASLH---FSLHIRDQSPDSALYLCAVSWTGGYKVVFGSGTRLIVSPD 132

RESULT 4
T-cell receptor alpha chain precursor V region (BTA25) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: F45893
R;Ishiguro, N.; Tanaka, A.; Shinagawa, M.
Immunogenetics 31, 57-60, 1990
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.
A:Reference number: A45893; MUID:90129157; PMID:2137108
A:Accession: F45893
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <ISH>
A:Cross-references: GB:D90015; NID:G217618; PID:BA44065.1; PID:G217619
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F;36-109/Domain: immunoglobulin homology <IMW>

Query Match 16.6%; Score 105; DB 2; Length 131;
Best Local Similarity 30.3%; Pred. No. 0.0025;
Matches 36; Conservative 23; Mismatches 34; Indels 26; Gaps 8;

QY 3 VSQPEIRTL-EGSSAFPCSFNASQGRLAIGSVTFRDEVPVGVK-----VRNGTPEF 55

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```

Db 24 VEQSPVLSQEGANSTLRCNFSDT-----VDSVQVFQCN--PGGALTTLFFIASGTKK- 75
QY 56 RGR LAPASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGT-----GNGTRLV 109
Db 76 NERMSVTNSK---ERYSTLHITASQLEDAATYLCVCAVD---LGSNGRQLVFGKGTSLAV 128

RESULT 5
A42692
T-cell receptor alpha chain (lysozyme peptide specific) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A42692
R;Kobori, J.A.; Hood, L.; Shaastri, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 2940-2944, 1992
A:Title: Structure-function relationship among T-cell receptors specific for lysozyme pe
A:Reference number: A42692; MUID:92212944; PMID:1313573
A:Accession: A42692
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOB>
A:Cross-references: GB:M87844; NID:G201804; PID:AAA51236.1; PID:G554375
A:Experimental source: T-cell hybrid BOH.9.1
A:Note: sequence extracted from NCBI backbone (NCBI:92850, NCBI:92851)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F;36-109/Domain: immunoglobulin homology <IMW>

Query Match 16.3%; Score 103; DB 2; Length 129;
Best Local Similarity 29.8%; Pred. No. 0.0039;
Matches 39; Conservative 14; Mismatches 34; Indels 44; Gaps 8;

QY 2 WVS-----OPPRTIRTEGSSAFPCSFNASQGRLAIGSVTFRDE-----VWPG 45
Db 18 WVGDKVKVQSPSALSLOEGTNSALRCNFS-----IAATTQVQFLQNPGRSLNLFYLPV- 71

QY 46 KEVRNGTPEPRGLAPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLGVGTGN- 103
Db 72 -----GTKE-NGRLKSAFDSK---ESYSTLHIRDQALEDSDGTIFYCAAE-----DTGNYK 116

QY 104 -----GTRLV 109
Db 117 YVFCAGTRLKV 127

RESULT 6
T-cell receptor alpha chain V region (5C.C7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: B24092
R;Fink, P.J.; Mattis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1988
A:Title: Correlations between T-cell specificity and the structure of the antigen recept
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: B24092
A:Molecule type: mRNA
A:Residues: 1-110 <FIN>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F;16-89/Domain: immunoglobulin homology <IMW>

Query Match 15.2%; Score 102.5; DB 2; Length 110;
Best Local Similarity 31.9%; Pred. No. 0.0037;
Matches 36; Conservative 16; Mismatches 46; Indels 15; Gaps 6;

QY 3 VSQPEIRTL-EGSSAFPCSFNASQGRLAIGSVTWF-----RDEVVPGKVRNGTPEFRG 57
Db 4 VEQSPSALSHEGTGSAALRCNFTTT-----MRAVQWFRKNSRGSGLNLFYIASGTKE-NG 57

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDAISYVCRVEVLGLG-VGTGNGTRLV 109

```

Db 58 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAEASNTNKVVGIGTRLQV 107

## RESULT 7

154487  
T-cell receptor alpha chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: F54487; 168823  
R:Nakajima, P.B.; Di Vincenzo, J.P.; Jameson, S.C.; Gascoigne, N.R.J.  
Immunogenetics 35, 190-198, 1992  
A>Title: Chromosome 14 in B10.A (18R) mice is recombinant and includes Tcr-a alleles.  
A:Reference number: F54487; MUID:92165347; PMID:1371499  
A:Accession: F54487  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-120 <RES>  
A:Cross-references: UNIPROT:Q31213; GB:M55634; NID:G199677; PIDN:AAA39701.1; PID:G199678  
A:Accession: 168823  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 104-120 <RES>  
A:Cross-references: GB:M55634; NID:G199677; PIDN:AAA39702.1; PID:G199679  
A>Note: J-alpha TA61  
C:Genetics:  
A:Gene: MHC-V-alpha-11; J-alpha-TA61  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: transmembrane protein  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 16.0%; Score 101; DB 2; Length 120;  
Best Local Similarity 31.6%; Pred. No. 0.0057;  
Matches 36; Conservative 17; Mismatches 47; Indels 14; Gaps 6;

QY 3 VSPPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---EVVPKKEVRNGTPEFRG 57

Db 14 VEQSPSALSHEGTGSLRCNFTTT-----MRVQVFRQNSRGLSLFLYASGTKE-NG 67

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGIVGTGNGTRLVVEKEHPOLG 110

Db 68 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAADNTNTKLTFGDGTVLTKV 119

## RESULT 8

D24092  
T-cell receptor alpha chain precursor V region (B10) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 01-Dec-2000 #text\_change 11-Jan-2002  
C:Accession: D24092; S03507  
R:Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A>Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A:Reference number: A93380; MUID:86230843; PMID:3012351  
A:Accession: D24092  
A:Molecule type: mRNA  
A:Residues: 1-131 <FIN>  
R:Winko, A.; Mjolsness, S.; Hood, L.  
Nature 316, 832-836, 1995  
A>Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.  
A:Reference number: S03503; MUID:85296332; PMID:2993908  
A:Accession: S03507  
A:Molecule type: DNA  
A:Residues: 111-130 <WIN>  
A:Cross-references: EMBL:G54519; NID:G54519; PIDN:CAA26864.1; PID:G1334131  
A>Note: this sequence was determined from the germline gene  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <WAT>  
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match 15.7%; Score 99.5; DB 2; Length 131;  
Best Local Similarity 29.3%; Pred. No. 0.0089;

Matches 36; Conservative 18; Mismatches 42; Indels 27; Gaps 7;

QY 3 VSPPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---RDEVVPKKEVRNGTPEFRG 57

Db 24 VEQSPSALSHEGTGSLRCNFTTT-----MRVQVFRQNSRGLSLFLYASGTKE-NG 77

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGIVGTGNGTRLVVEKEHPOLG 117

Db 78 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAE-----ATSSGQKLV-----FG 121

QY 118 AGT 120

Db 122 QGT 124

## RESULT 9

E24092  
T-cell receptor alpha chain precursor V region (4.C3) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C:Accession: E24092  
R:Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A>Title: Correlations between T-cell specificity and the structure of the antigen recep  
A:Reference number: A93380; MUID:86230843; PMID:3012351  
A:Accession: E24092  
A:Molecule type: mRNA  
A:Residues: 1-131 <FIN>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-131/Product: T-cell receptor alpha chain V region 4.C3 #status predicted <WAT>  
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match 15.7%; Score 99.5; DB 2; Length 131;  
Best Local Similarity 29.3%; Pred. No. 0.0089;

Matches 36; Conservative 18; Mismatches 42; Indels 27; Gaps 7;

QY 3 VSPPEIRTL-EGSSAFPCSFNASQGLAIGSVTWTFD---RDEVVPKKEVRNGTPEFRG 57

Db 24 VEQSPSALSHEGTGSLRCNFTTT-----MRVQVFRQNSRGLSLFLYASGTKE-NG 77

QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGIVGTGNGTRLVVEKEHPOLG 117

Db 78 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAE-----STSSGQKLV-----FG 121

QY 118 AGT 120

Db 122 QGT 124

## RESULT 10

RWMSAV  
T-cell receptor alpha chain precursor V region (2B4) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 09-Jul-2004  
C:Accession: A02015  
R:Chien, Y.; Becker, D.M.; Lindsten, T.; Okamura, M.; Cohen, D.I.; Davis, M.M.  
Nature 312, 31-35, 1984  
A>Title: A third type of murine T-cell receptor gene.  
A:Reference number: A93344; MUID:85036634; PMID:6548551  
A:Accession: A02015  
A:Molecule type: mRNA  
A:Residues: 1-132 <CHI>  
A:Cross-references: UNIPROT:P01739  
A:Experimental source: hybridoma 2B4, clone T11  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein; heterotetramer; receptor; T-cell  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-132/Product: T-cell receptor alpha chain V region (2B4) #status predicted <WAT>  
F:21-113/Region: V segment  
F:114-117/Region: D segment  
F:118-132/Region: J segment

F;42/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 99; DB 1; Length 132;  
Best Local Similarity 29.4%; Pred. No. 0.01;  
Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;

QY 3 VSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTFWFRDEVPVPGKEVR-----NGTPE 54

Db 24 VQSPESLIPEGARTSLNCTFSDASQY-----FWYRQH--SGKAPKALMIFNGEKE 77

QY 55 FRCLAPLASSRFLHDHQAELHIRDVRGHDAISIVCRVEVLGLGVGTNGTRLVVEKEHP 114

Db 78 -EGRFTHLNKASH--FSLHIRDSPQSDSALYLCAVTLYG-----GSGNKLI----- 122

QY 115 QLCAGT 120

Db 123 -FGTGT 127

# RESULT 11

A31211

T-cell receptor alpha chain precursor V region (V11.3-J39) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-Jul-1999

C;Accession: A31211

R;Malissen, M.; Trucy, J.; Letourneur, F.; Rebai, N.; Dunn, D.E.; Fitch, F.W.; Hood, L.

Cell 55, 49-59, 1988

A;Title: A T cell clone expresses two T cell receptor alpha genes but uses one alpha-bed

A;Reference number: A94656; MUID:89003051; PMID:3262424

A;Accession: A31211

A;Molecule type: DNA

A;Residues: 1-130 <NAL>

A;Cross-references: GB:M22603; NID:G340716; PIDN:AAA63777.1; PID:G710556

C;Genetics: 18/1

A;Introns: 18/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

F;36-109/Domain: immunoglobulin homology <IMV>

Query Match 15.6%; Score 98.5; DB 2; Length 130;  
Best Local Similarity 30.6%; Pred. No. 0.01;  
Matches 39; Conservative 15; Mismatches 42; Indels 29; Gaps 8;

QY 2 WVS-----QPPRTLEGSSAFPCSFNASQGRLAIGSVTFWFRDEVPVPGKEVRN----- 50

Db 18 WVSQDKVKQSPSALSQEGTNSALRCNFS-----IAATTQVFLQN--PRGSLMNLFLYL 70

QY 51 -GTFEPRGLAPLASSRFLHDHQAELHIRDVRGHDAISIVCRVEVLGLGVGT-----GNGT 105

Db 71 PGTK-NGRLKSAFDSK---ESYSTLHIRDAQLDSGTGYFCAAG--CGNSGYQRFGTGT 124

QY 106 RLVV 109

Db 125 KLQV 128

# RESULT 12

S26408

T-cell receptor beta chain V region (5.5) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C;Accession: S26408

R;Bowman, S.J.; Lanchbury, J.S.

submitted to the EMBL Data Library, September 1992

A;Description: T cell receptor beta chain sequences from patients with rheumatoid arthri

A;Reference number: S26408

A;Accession: S26408

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-146 <BOW>

A;Cross-references: EMBL:X58527; NID:G36172; PIDN:CAA48540.1; PID:G36173

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

F;35-112/Domain: immunoglobulin homology <IMV>

Query Match 15.6%; Score 98.5; DB 2; Length 146;  
Best Local Similarity 26.0%; Pred. No. 0.013;  
Matches 33; Conservative 23; Mismatches 44; Indels 27; Gaps 6;

QY 3 VSQPE-IRTEGSSAFPCSFNASQGRLAIGSVTFWFRDEVPVPG-----KEYRNGT 52

Db 23 VIQFTHLIKT-RQQVTLRCSSQSGH-----NTVSWYQALQGQPFQYYREENG- 75

QY 53 PEPRGLAPLASSRFLHDHQAELHIRDVRGHDAISIVCRVEVLGLGVGT-----GNGT 105

Db 76 --RGNPPFRFGLOPFNYSSSELNVNVALELDDSALYCASSFKGLGLPSRGVQYFGPGT 132

QY 106 RLVEKE 112

Db 133 RLTVTD 139

# RESULT 13

S36325

T-cell receptor delta chain precursor - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000

C;Accession: S36325; S23040

R;Hein, W.R.; Dudley, L.

EMBO J. 12, 715-724, 1993

A;Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta

A;Reference number: S36287; MUID:93178447; PMID:8440261

A;Accession: S36325

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-139 <HBI>

A;Cross-references: EMBL:Z12997; NID:G2258; PIDN:CAA78341.1; PID:G2259

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

F;33-113/Domain: immunoglobulin homology <IMV>

Query Match 15.3%; Score 97; DB 2; Length 139;  
Best Local Similarity 30.6%; Pred. No. 0.017;  
Matches 37; Conservative 10; Mismatches 52; Indels 22; Gaps 6;

QY 7 PEIRTEGSSAFPCSFNASQGRLAIGSVTFWR---DEVVPGKEVRNGTPEFGRLAPLA 63

Db 26 PEQVAVSGREVTLOCTFQTYSN---PDLYWYKTPDAVQFVLYRDNT---RSRDADFA 79

QY 64 SSRFLHDHQA-----ELHIRDVRGHDAISIVCRVEVLGLGV-----GTGNGTRLVVEK 111

Db 80 RGRFTVQHSVRSKTFHLVISSVRPEDTAVYCALD-LQGIYDTDKLTFGKGTFLIVEP 138

QY 112 E 112

Db 139 E 139

# RESULT 14

B47712

myelin/oligodendrocyte glycoprotein - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jan-1994 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004

C;Accession: B47712

R;Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roessel, N.

Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993

A;Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunoglobul

A;Reference number: A47712; MUID:93376728; PMID:8367453

A;Accession: B47712

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-218 <PHA>

A;Cross-references: UNIPROT:Q63345

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:137804)

C;Genetics:



Search completed: November 16, 2004, 19:15:51  
Job time : 24.8276 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 134.005 seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LWSVQPEIRTELEGSFAFLP.....TGNGLRVVKEHPQLGACT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632	100.0	201	1 NCT3 HUMAN	014931 homo sapien
2	624	98.7	201	1 NCT3_PANTR	P61484 pan troglod
3	599	94.8	176	1 NCT3_MACFA	P61483 macaca fasc
4	599	94.8	180	1 NCT3_MACMU	Q8m102 macaca mula
5	424	67.1	192	1 NCT3 RAT	Q8cfd9 rattus norv
6	108.5	17.2	272	2 Q7Q1Q2	Q7g1g2 anopheles g
7	108.5	17.2	449	2 Q9NKA5	Q9nka5 drosophila
8	105.5	16.7	235	2 Q9NM11	Q9nm11 mus musculu
9	103	16.3	329	2 Q8N225	Q8n225 homo sapien
10	103	16.3	1340	2 Q8N2A2	Q8n2a2 homo sapien
11	102	16.1	172	2 Q71AW3	Q71aw3 bos taurus
12	102	16.1	172	2 AAQ10930	AAQ10930 bos tauru
13	101.5	16.1	221	2 Q28090	Q28090 bos taurus
14	100.5	15.9	221	2 Q97631	Q97631 ovis aries
15	99	15.7	132	1 TVA2 MOUSE	P01739 mus musculu
16	98.5	15.6	273	2 Q6PZ28	Q6piz8 homo sapien
17	98.5	15.6	273	2 AAH5727	AAH5727 homo sapi
18	98	15.5	313	2 Q6IPU1	Q6ipul homo sapien
19	98	15.5	313	2 AAH71724	AAH71724 homo sapi
20	97.5	15.4	240	2 Q6MG96	Q6mg96 rattus norv
21	97.5	15.4	240	2 CAE83950	CAE83950 rattus no
22	96.5	15.3	350	2 Q9VFU7	Q9vfuf drosophila
23	95.5	15.1	245	1 MCG RAT	Q63345 rattus norv
24	95.5	15.1	245	2 Q6MFX9	Q6mfx9 rattus norv
25	95.5	15.1	245	2 CAE84068	CAE84068 rattus no
26	94	14.9	526	1 BUTY HUMAN	Q13410 homo sapien
27	94	14.9	526	2 Q9H458	Q9h458 homo sapien
28	93.5	14.8	246	1 MCG MOUSE	Q61885 mus musculu
29	93.5	14.8	274	2 Q80YU5	Q80yu5 mus musculu
30	93	14.7	1694	1 SN_MOUSE	Q62230 mus musculu
31	92.5	14.6	223	2 Q7TMX1	Q7tmx1 mus musculu

32	92	14.6	174	2	Q9Z1A7	Q9z1a7 rattus norv
33	91.5	14.5	223	2	Q9TT02	Q9tt02 canis famil
34	91.5	14.5	223	2	Q9GKP2	Q9gkp2 canis famil
35	91.5	14.5	223	2	Q62859	Q62859 rattus norv
36	90.5	14.3	272	2	Q70356	Q70356 mus musculu
37	90.5	14.3	600	2	Q7FN36	Q7fn36 anopheles g
38	90	14.2	524	2	Q921K7	Q921k7 mus musculu
39	90	14.2	700	2	Q7TSU7	Q7tsu7 mus musculu
40	90	14.2	700	2	BAC33658	Bac33658 m es cell
41	89.5	14.2	137	2	Q95653	Q95653 homo sapien
42	89	14.1	108	2	Q8UJ25	Q8uj25 orectolobus
43	89	14.1	717	2	Q7PUQ1	Q7puq1 anopheles g
44	88.5	14.0	223	1	CTL4 MOUSE	P09793 mus musculu
45	88.5	14.0	223	2	Q9XSY7	Q9xsy7 felis silve

#### ALIGNMENTS

RESULT 1  
NCT3 HUMAN  
ID NCT3 HUMAN STANDARD; PRT; 201 AA.  
AC 014931; 014930; 014932; 095667; 095668; 095669;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3; Synonyms=1C7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD3Z, AND FUNCTION.  
RC TISSUE=Lymphoid;  
RX PubMed=10562324;  
RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaspina A., Biassoni R., Bottino C., Moretta L., Moretta A.;  
RT "Identification and molecular characterization of NKP30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells.";  
RL J. Exp. Med. 190:1505-1516(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD3Z.  
RC TISSUE=Peripheral blood;  
RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K., Juji T.;  
RT "Identification of two novel single nucleotide polymorphisms in the NKP30 gene in human natural killer cells.";  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RX MEDLINE=99219514; PubMed=10202016;  
RA Neville M.J., Campbell R.D.;  
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among the predicted products of novel genes close to the TNF locus in the human MHC.";  
RL J. Immunol. 162:4745-4754(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC TISSUE=Spleen;  
RX MEDLINE=96422187; PubMed=8824804;  
RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
RT "Genes in a 220-kb region spanning the TNF cluster in human MHC.";  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=14656967; DOI=10.1101/gr.1736803;  
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,



RA TISSUE=Lymphoid;  
RA Biassoni R.;  
RT "Characterization of natural killer receptors in chimpanzees.";  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD3Z (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
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CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
CC  
CC EMBL; AJ516006; CAD56759.1; -.  
CC PROSITE; PS0835; IG LIKE; 1.  
CC Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC SIGNAL 1 18 Potential.  
CC CHAIN 19 201 Natural cytotoxicity triggering receptor  
CC FT DOMAIN 19 135 Extracellular (Potential).  
CC FT TRANSMEM 136 156 Potential.  
CC FT DOMAIN 157 201 Cytoplasmic (Potential).  
CC FT DOMAIN 19 126 IG-like.  
CC FT DISULFID 39 108 By similarity.  
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
CC SQ SEQUENCE 201 AA; 21656 MW; 3768ACC768BD749 CRC64;  
  
CC Query Match 98.7%; Score 624; DB 1; Length 201;  
CC Best Local Similarity 99.2%; Pred. No. 1.2e-55;  
CC Matches 119; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
CC QY 1 LWSQPEIRTELEGSAFLPCSFNASQRLAIGSVTFRDEVVPGKEVRNGTPEFRGLA 60  
CC Db 19 LWSQPEIRTELEGSAFLPCSFNASQRLAIGSVTFRDEVVPGKEVRNGTPEFRGLA 78  
CC QY 61 PLASSRFLHQAEHLHVRDVGHDASIVYCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 120  
CC Db 79 PLASSRFLHQAEHLHVRDVGHDASIVYCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 138  
  
CC RESULT 3  
CC ID NCT3 MACFA STANDARD; PRT; 176 AA.  
CC AC P61483; Q95JB8;  
CC DT 05-JUL-2004 (Rel. 44, Created)  
CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
CC DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
CC cell p30-related protein) (NKp30) (NK-p30).  
CC GN Name=NCR3;  
CC OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
CC OC Cercopithecinae; Macaca.  
CC OX NCBI\_TaxID=9541;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RC TISSUE=Lymphoid;  
CC RA Rizzi M., Biassoni R.;  
CC RT "Non MHC specific natural cytotoxicity receptors (NCR) expressed in  
CC Macaca fascicularis lymphoid cells.";  
CC RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC

CC -!- SUBUNIT: Interacts with CD3Z (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC  
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CC or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
CC  
CC EMBL; AJ278389; CAC41081.1; -.  
CC HSP; P16410; I185.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; IG; 1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS0835; IG LIKE; 1.  
CC Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
CC SIGNAL 1 18 Potential.  
CC CHAIN 19 176 Natural cytotoxicity triggering receptor  
CC FT DOMAIN 19 135 Extracellular (Potential).  
CC FT TRANSMEM 136 156 Potential.  
CC FT DOMAIN 157 176 Cytoplasmic (Potential).  
CC FT DOMAIN 19 126 IG-like.  
CC FT DISULFID 39 108 By similarity.  
CC FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
CC FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
CC SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;  
  
CC Query Match 94.8%; Score 599; DB 1; Length 176;  
CC Best Local Similarity 95.0%; Pred. No. 3.8e-53;  
CC Matches 114; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
CC QY 1 LWSQPEIRTELEGSAFLPCSFNASQRLAIGSVTFRDEVVPGKEVRNGTPEFRGLA 60  
CC Db 19 LWSQPEIRTELEGSAFLPCSFNASQRLAIGSVTFRDEVVPGKEVRNGTPEFRGLA 78  
CC QY 61 PLASSRFLHQAEHLHVRDVGHDASIVYCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 120  
CC Db 79 PLASSRFLHQAEHLHVRDVGHDASIVYCRVEVLGVGTGNGTRLVVEKEHPOLGAGT 138  
  
CC RESULT 4  
CC ID NCT3 MACMU STANDARD; PRT; 180 AA.  
CC AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
CC DT 05-JUL-2004 (Rel. 44, Created)  
CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
CC DT 01-OCT-2004 (Rel. 45, Last annotation update)  
CC DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
CC cell p30-related protein) (NKp30) (NK-p30).  
CC GN Name=NCR3;  
CC OS Macaca mulatta (Rhesus macaque).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
CC OC Cercopithecinae; Macaca.  
CC OX NCBI\_TaxID=9544;  
CC RN [1]  
CC RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
CC RA LaBonte M.L., Miller J., Letvin N.L.;  
CC RT "Molecular cloning of rhesus monkey NKp46 and NKp30 and identification  
CC of NKp46SD and NKp30S.";  
CC RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis (By similarity).  
CC





RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,  
 RA Butenheff C., Champagne M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,  
 RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,  
 RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,  
 RA Lewis S., Li P., Lonotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,  
 RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,  
 RA Sechi H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,  
 RA Zieran L.D., Rubin G.M.,  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003411; AA044902.1; -  
 DR Flybase; FBgn028914; CG15275.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SMO0409; ig; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 449 AA; 50945 MW; 162A631C0C172154 CRC64;  
 Query Match 17.2%; Score 108.5; DB 2; Length 449;  
 Best Local Similarity 33.0%; Pred. No. 0.016;  
 Matches 33; Conservative 11; Mismatches 35; Indels 21; Gaps 5;  
 Qy 8 EIRTEGSSAFPCSFNAGSLAIGSVTFWRD-----VPGKEVRN-----GTPE 54  
 Db 32 DIDAVEGKSVSLPCPIPEPLDNVYM--VLWFRNAGIPLYSFVDRKESQPRHWSAPE 89  
 Qy 55 FRGLAPLASSRFLHDHQ-RLHIRDVRGHDASIVYCVSE 93  
 Db 90 VFG-----SRKHFDSQPATLEIKOIKRHDQGIYCRVD 124  
 RESULT 8  
 Q99M11 PRELIMINARY; PRT; 235 AA.  
 AC Q99M11;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Czech II;  
 RC TISSU=Mammary tumor metastatized to lung. Tumor arose spontaneously;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Joquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalski U., Small D.E., Schnerk A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Czech II;  
 RC TISSU=Mammary tumor metastatized to lung. Tumor arose spontaneously;

RA Strausberg R.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002129; AA02129.1; -  
 DR HSP; P01843; 1UNH.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; CI-set; 1.  
 DR Pfam; PF00047; ig; 1.  
 DR SMART; SMO0406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 235 AA; 25403 MW; 39807BF6782A3FB CRC64;  
 Query Match 16.7%; Score 105.5; DB 2; Length 235;  
 Best Local Similarity 28.8%; Pred. No. 0.016;  
 Matches 34; Conservative 22; Mismatches 43; Indels 19; Gaps 5;  
 Qy 1 LWVSQPPPIRTLEGSSAFPCSFNAGSLAIGSVTFWRD-----EVVPGKEVRNG-- 51  
 Db 21 LVLTQPSVSISLSTAKLPC--KASTGNIGDSVYVWYQQYMGSPINMIYGDRLRSGV 78  
 Qy 52 TPEFRGLAPLASSRFLHDHQ-RLHIRDVRGHDASIVYCVSEVGLGVGTNGRLVY 109  
 Db 79 SDRFSGSIDSSNGAF-----LTQNVQADDEADYVQSYSSGIRV-FGGGTLTV 128  
 RESULT 9  
 Q8N225 PRELIMINARY; PRT; 329 AA.  
 AC Q8N225;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein FLJ36264.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSU=Thymus;  
 RX PubMed=14702039;  
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,  
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 RA Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,  
 RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,  
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuna M., Shiratori A.,  
 RA Sudo H., Hosoiri T., Kaku Y., Kodaera H., Kondo H., Sugawara M.,  
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,  
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,  
 RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,  
 RA Tanai H., Kinata M., Watanabe M., Hiraoa K., Chiba Y., Ishida S.,  
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Nomura J.,  
 RA Kaneshori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,  
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,  
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,  
 RA Yoshikawa K., Yutani K., Ichihara T., Shiohata N., Sano S.,  
 RA Moriya S., Motomura H., Satoh N., Takami S., Terashima Y., Suzuki O.,  
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,  
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,  
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,  
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,  
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y.,  
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,  
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,  
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,  
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,  
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,  
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,  
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;



DE	CTLA-4 isoform 1.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Ahn J.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF539438; AAQ10930.1; -.
DR	InterPro; IPR008096; CTIA4.
DR	InterPro; IPR003599; IG.
DR	InterPro; IPR007110; IG-like.
DR	InterPro; IPR003596; IG_v.
DR	Pfam; PF00047; IG; 1.
DR	PRINTS; PRCL720; CTLANTIGEN4.
DR	SMART; SMO0409; IG; 1.
DR	SMART; SMO0406; IGV; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
SQ	SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;
Query Match	16.1%; Score 102; DB 2; Length 172;
Best Local Similarity	30.8%; Pred. No. 0.026;
Matches	36; Conservative 18; Mismatches 55; Indels 8; Gaps 4
QY	3 VSQPSEITLEGSAFLPCSFNASGRLAIGSVTFWFRDEVVPGKEVRNGTPEFRGLAPL 62
Db	38 VTQPPVLASSRGVASCEYESS-GKADEVRTVTLREAGSQVTEVCAGTYMVEDELTF 96
QY	63 ASSRFL---HDHQELHIRDVRGHDAIYVCRVEVL---GLGVGTGNTRL-VVEKE 112
Db	97 DDSICIGTSRGNKYNLTIQGLRAMDTGLYVCKVELMYPPPYVVVGINGTGTVIIAKE 153
RESULT 12	
AAQ10930	PRELIMINARY; PRT; 172 AA.
ID	AAQ10930;
AC	AAQ10930;
DT	02-MAR-2004 (TrEMBLrel. 27, Created)
DT	02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT	02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE	CTIA-4 isoform 1.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID=9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Ahn J.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF539438; AAQ10930.1; -.
SQ	SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;
Query Match	16.1%; Score 102; DB 2; Length 172;
Best Local Similarity	30.8%; Pred. No. 0.026;
Matches	36; Conservative 18; Mismatches 55; Indels 8; Gaps 4
QY	3 VSQPSEITLEGSAFLPCSFNASGRLAIGSVTFWFRDEVVPGKEVRNGTPEFRGLAPL 62
Db	38 VTQPPVLASSRGVASCEYESS-GKADEVRTVTLREAGSQVTEVCAGTYMVEDELTF 96
QY	63 ASSRFL---HDHQELHIRDVRGHDAIYVCRVEVL---GLGVGTGNTRL-VVEKE 112
Db	97 DDSICIGTSRGNKYNLTIQGLRAMDTGLYVCKVELMYPPPYVVVGINGTGTVIIAKE 153
RESULT 13	
Q28090	PRELIMINARY; PRT; 221 AA.
ID	Q28090
AC	Q28090;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE CTLA-4 protein precursor.  
 GN Name=CTLA-4;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP MEDLINE=96186531; PubMed=8606060;  
 RA Parsons K.R., Young J.R., Collins R.A., Howard C.J.;  
 RT "Cattle CTLA-4, cattle CD28 and chicken CD28 bind human CD86 (B70);  
 RL although the MYPPPY hexapeptide is not conserved in cattle CD28.";  
 DR EMBL; X93305; CAA63708.1; -.  
 DR HSP; P16410; I185.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR008096; CTLA4.  
 DR InterPro; IPR003599; Ig.  
 DR Pfam; PF00047; Ig; 1.  
 DR PRINTS; PR01720; CTLANTIGEN4.  
 DR SMART; SM00409; Ig; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Signal.  
 FT SIGNAL 1 35 Potential.  
 SQ SEQUENCE 221 AA; 24433 MW; 2CAFL48422C597AA CRC64;  
 Query Match 16.1%; Score 101.5; DB 2; Length 221;  
 Best Local Similarity 29.7%; Pred. No. 0.039;  
 Matches 35; Conservative 17; Mismatches 59; Indels 7; Gaps 3;  
 QY 3 VSQPEIRTELGSAFLPCSNASQGRLAIGSVTWFRDEVVPGKEVNGTPEFRGLAPL 62  
 Db VTQPPVVLASSRGVASFCEYSS-GKADEVRTVLKAGIQVTEVCAGTYVVEDELTEL 96  
 QY 63 ASSEFL---HDHQAEHLIRVGRGHDAIYVCRVEVL---GLGVGTGNGTGLVVEKEHP 114  
 Db DDSTCIGTSRGNKVNLTIGLRAMDTGLYVCKVELMPPPPYVGGNGTQIYVIDPEP 154  
 RESULT 14  
 ID O97631 PRELIMINARY; PRT; 221 AA.  
 AC O97631;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytotoxic T-lymphocyte-associated protein 4.  
 GN Name=CTLA-4;  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP MEDLINE=99309828; PubMed=10380709;  
 RA Chaplin P.J., Pietrala L.N., Scheerlinck J.P.;  
 RT "Cloning and sequence comparison of sheep CD28 and CTLA-4.";  
 RL Immunogenetics 49:583-584(1999).  
 DR EMBL; AF092740; AAD04380.1; -.  
 DR HSP; P16410; I185.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR008096; CTLA4.  
 DR InterPro; IPR003599; Ig.  
 DR Pfam; PF00047; Ig; 1.  
 DR PRINTS; PR01720; CTLANTIGEN4.

DR SMART; SM00409; IG; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 SQ SEQUENCE 221 AA; 24490 MW; D317B9D5557BA6FB CRC64;  
 Query Match 15.9%; Score 100.5; DB 2; Length 221;  
 Best Local Similarity 28.8%; Pred. No. 0.049;  
 Matches 34; Conservative 18; Mismatches 59; Indels 7; Gaps 3;  
 QY 3 VSQPEIRTELGSAFLPCSNASQGRLAIGSVTWFRDEVVPGKEVNGTPEFRGLAPL 62  
 Db VTQPPVVLASSRGVASFCEYSS-GKADEVRTVLKAGIQVTEVCAGTYVVEDELTEL 96  
 QY 63 ASSEFL---HDHQAEHLIRVGRGHDAIYVCRVEVL---GLGVGTGNGTGLVVEKEHP 114  
 Db DDSTCIGTSRGNKVNLTIGLRAMDTGLYVCKVELMPPPPYVGGNGTQIYVIDPEP 154  
 RESULT 15  
 ID TVA2 MOUSE STANDARD; PRT; 132 AA.  
 AC P01739;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE T-cell receptor alpha chain V region 2B4 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (CLONE TT11).  
 RA MEDLINE=85036634; PubMed=6548551;  
 RA Chien Y., Becker D.M., Lindsten T., Okamura M., Cohen D.I.,  
 RA Davis M.M.;  
 RT "A third type of murine T-cell receptor gene.";  
 RL Nature 312:31-35(1984).  
 DR PIR; A02015; RWSAV.  
 DR HSP; P01738; 1TCR.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell.  
 FT SIGNAL 1 20  
 FT CHAIN 21 132 T-cell receptor alpha chain V region 2B4.  
 FT DOMAIN 21 113 V segment.  
 FT DOMAIN 114 117 D segment.  
 FT DOMAIN 118 132 J segment.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...).  
 FT NON\_TER 132 132  
 SQ SEQUENCE 132 AA; 14668 MW; CABBF6CF1DD3448B CRC64;  
 Query Match 15.7%; Score 99; DB 1; Length 132;  
 Best Local Similarity 29.4%; Pred. No. 0.04;  
 Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;  
 QY 3 VSQPEIRTELGSAFLPCSNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPE 54  
 Db VQSPESLIIVPEGARTSLNCTFSDASQY----FWYRQH--SGKAPKALMSIFSNGEKE 77  
 QY 55 FRGLAPLASSRFLHDHQAEHLIRVGRGHDAIYVCRVEVLGLGVGTGNGTGLVVEKEHP 114  
 Db EGRFTIHLNKASLH---FSLHIRDSPSALFLCAVTLYG-----GSGNKLI----- 122  
 QY 115 QLQAGT 120  
 Db 123 -FGTGT 127  
 Search completed: November 16, 2004, 19:14:30  
 Job time : 135.205 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 127,639 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-4  
Perfect score: 632  
Sequence: 1 LWSQPEIRTLGSSAFLP.....TGNQTRLVVEKEHPQLGAGT 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	632	100.0	120	4 AAE02771	Human Nkp
2	632	100.0	120	8 ADQ30924	Human Nkp
3	632	100.0	177	2 AAY06402	Human B-c
4	632	100.0	190	2 AAY06401	Human B-c
5	632	100.0	190	4 AAE02769	Human Nkp
6	632	100.0	190	8 ADO19810	Human PRO
7	632	100.0	190	8 ADQ30923	Human Nkp
8	632	100.0	201	2 AAY06403	Human B-c
9	617	97.6	135	5 AAE19109	Human Nkp
10	617	97.6	369	5 AAE19110	Human Nkp
11	607	96.0	382	8 ADP48750	Human Nkp
12	118.5	18.8	138	3 AAU75565	Murine T
13	105.5	16.7	138	4 AAM24182	Rhesus mo
14	105	16.6	140	4 AAB68882	Human REC
15	104	16.5	262	2 AAR97726	B10 singl
16	103	16.3	136	4 ABB11287	Human mem
17	103	16.3	329	7 ADB55555	Human pro
18	103	16.3	3931	6 ABU07377	Human pro
19	103	16.3	3931	7 ADG39786	Human nov
20	101.5	16.1	267	2 AAU04300	Murine T-
21	100.5	15.9	273	7 ADI60192	Secrated
22	99	15.7	246	5 AAE20273	Human lun
23	99	15.7	270	1 AAP50256	Sequence
24	98.5	15.6	252	5 ABP45484	Human Bly
25	98.5	15.6	252	7 ADG96311	Single ch

26	98.5	15.6	740	4 ABG28146	Novel hum
27	97.5	15.4	216	5 ABP58185	CTLA-4-GC
28	96.5	15.3	125	5 ABP52181	Human mon
29	96.5	15.3	350	4 ABB69289	Drosophil
30	95.5	15.1	131	6 AAO29772	Rat myeli
31	95.5	15.1	150	2 AAU97817	Rat myeli
32	95.5	15.1	218	8 ADO05888	Rat MOG p
33	94	14.9	526	2 AAU97814	Human but
34	94	14.9	526	5 AAO15804	Human but
35	94	14.9	526	7 ADJ69867	Human hea
36	92.5	14.6	235	5 AAG64474	Human typ
37	92.5	14.6	388	5 ABB07681	MOG-Pc fu
38	92.5	14.6	388	6 ADA14289	Mutated M
39	92.5	14.6	388	6 ADA14265	Human imm
40	92	14.6	174	3 AAB08208	Amino aci
41	91.5	14.5	223	2 AAU41083	Canine CT
42	91.5	14.5	268	2 AAR77288	T-cell re
43	91.5	14.5	269	3 AAY69995	Human rec
44	91	14.4	205	2 AAY41173	Llama-Vhh
45	91	14.4	253	5 ABP45534	Human Bly

ALIGNMENTS

RESULT 1

AAE02771  
ID AAE02771 standard; protein; 120 AA.

XX AAE02771;

XX 06-AUG-2001 (first entry)

XX Human Nkp30 receptor extracellular region sequence.

Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
therapy; extracellular region.

XX Homo sapiens.

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02298307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

Novel compound, useful for detection and/or quantifying the presence of  
NK cells, comprises the amino acid sequences of the Nkp30 molecule.

Claim 1; Fig 7B; 83pp; English.

The invention relates to human Nkp30 receptor and its corresponding cDNA  
molecule which is involved in natural cytotoxicity mediated by natural  
killer (NK) cells and antibodies that identify the same. Nkp30 receptor  
is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
useful for detecting and/or quantifying the presence of NK cells in a  
biological sample. The invention also provide kits for detecting and/or  
quantifying the presence of NK cells, for the selective removal of NK  
cells from a biological sample, for the positive and selective  
purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a  
CC pharmaceutical composition which is used as a drug for grafting  
CC enhancement, graft versus host (GVH) inhibition, stimulation of graft  
CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma and/or  
CC microorganism, notably viral infection. NKp30 antibodies are useful for  
CC identifying NKp30 natural ligands and allow assessment of the level of  
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence NKp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is the extracellular region of human NKp30 receptor  
XX  
SQ Sequence 120 AA;

Query Match 100.0%; Score 632; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
Db 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

Qy 61 PLASSRFLHDHQAEHLHVRDVGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120  
Db 61 PLASSRFLHDHQAEHLHVRDVGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120

RESULT 2  
ADQ30924  
ID ADQ30924 standard; protein; 120 AA.  
XX  
AC ADQ30924;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human NKp30 extracellular region.  
XX  
KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
XX  
OS Homo sapiens.  
XX  
FN WO2004056392-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-EP014716.  
XX  
PR 23-DEC-2002; 2002US-0435344P.  
XX  
PA (INNA-) INNATE PHARMA.  
XX  
PI Romagne F, Andre P;  
XX  
DR WPI; 2004-507595/48.  
XX  
XX Pharmaceutical compositions that stimulate proliferation of natural  
XX killer cells useful for therapy of melanoma, chronic myeloid, and  
XX leukemia, comprise an anti-natural killer cell receptor antibody and  
XX interleukins.  
XX  
PS Claim 3; SEQ ID NO 2; 35pp; English.  
XX

The present sequence is that of the extracellular region of human NKp30  
CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
CC pharmaceutical compositions that have a stimulating effect on the  
CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
CC antibody(ies) and cytokine(s) being administered together or separately  
CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
CC antigen-binding fragment which specifically binds to NKp30 or to a

CC fragment, including the extracellular region, of NKp30. The  
CC pharmaceutical compositions, when used for daily subcutaneous injection,  
CC comprising from 1 mg to 100 mg/kg (body weight) of antibody(ies), and  
CC lower than 1 million units/square meter/day of cytokine(s), are useful  
CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,  
CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
XX prevention, palliation and therapy (claimed).

SQ Sequence 120 AA;

Query Match 100.0%; Score 632; DB 8; Length 120;  
Best Local Similarity 100.0%; Pred. No. 2e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
Db 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60

Qy 61 PLASSRFLHDHQAEHLHVRDVGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120  
Db 61 PLASSRFLHDHQAEHLHVRDVGHDASIVYCRVEVLGLGVGTGNGTRLVWEKEHPQLGAGT 120

RESULT 3  
AA06402  
ID AA06402 standard; protein; 177 AA.  
XX  
AC AA06402;  
XX  
DT 20-SEP-1999 (first entry)  
XX  
DE Human B-cell myelin oligodendrocyte glycoprotein EMOG.  
XX  
KW MBQG; B-cell myelin oligodendrocyte glycoprotein; human;  
KW signal transduction; immunomodulator; antiinflammatory;  
KW autoimmune disease; inflammation; gene therapy; diagnosis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..12  
FT Protein /note= "leader peptide"  
FT Modified-site /note= "mature protein"  
FT Modified-site 42  
FT Modified-site /note= "N-glycosylated"  
FT Modified-site 68  
FT Modified-site /note= "N-glycosylated"  
FT Domain /note= "N-glycosylated"  
FT Peptide 139..162  
FT Peptide 166..177  
FT /note= "transmembrane domain"  
FT /note= "alternatively spliced C-terminal end"

WC923867-A2.  
XX  
XX 20-MAY-1999.  
XX  
XX 05-NOV-1998; 98WO-US023826.  
XX  
XX 07-NOV-1997; 97US-0064761P.  
XX  
XX (BIOJ ) BIOGEN INC.  
XX  
XX Browning J;  
XX  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59348.  
XX  
XX Novel B-cell myelin oligodendrocyte glycoproteins.

PS Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre  
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX SQ Sequence 177 AA;

Query Match 100.0%; Score 632; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-62;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPEIRTLGSSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 78

QY 61 PLASSRFLHDQAEHLHIRDVRGHDASIYVCVRVEVLGLGVGTGNGTRLVVEKEHPOLGAGT 120  
 DB 79 PLASSRFLHDQAEHLHIRDVRGHDASIYVCVRVEVLGLGVGTGNGTRLVVEKEHPOLGAGT 138

RESULT 4

AAV06401  
 ID AAY06401 standard; protein; 190 AA.

XX AC AAY06401;

XX DT 20-SEP-1999 (first entry)

XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.

XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..12 /note= "leader peptide"

FT Protein 13..190 /note= "mature protein"

FT Modified-site 42 /note= "N-glycosylated"

FT Modified-site 68 /note= "N-glycosylated"

FT Modified-site 121 /note= "N-glycosylated"

FT Domain 139..162 /note= "transmembrane domain"

FT Peptide 166..190 /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

DR N-PSDB; AAX59347.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 2; Page 42; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre  
 CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX SQ Sequence 190 AA;

Query Match 100.0%; Score 632; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
 Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPEIRTLGSSAFLPCSFNASQGRLAIGSVTWFRDEVPGKEVRNGTPEFRGLA 78

QY 61 PLASSRFLHDQAEHLHIRDVRGHDASIYVCVRVEVLGLGVGTGNGTRLVVEKEHPOLGAGT 120  
 DB 79 PLASSRFLHDQAEHLHIRDVRGHDASIYVCVRVEVLGLGVGTGNGTRLVVEKEHPOLGAGT 138

RESULT 5

AAE02769  
 ID AAE02769 standard; protein; 190 AA.

XX AC AAE02769;

XX DT 06-AUG-2001 (first entry)

XX DE Human Nkp30 receptor.

XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
 KW therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..18 /label= "Signal\_peptide"

FT Protein 19..190 /label= "Mature\_Nkp30\_receptor\_protein"

FT Region 19..138 /label= "Extracellular region"

FT /note= "Forms an immunoglobulin (Ig) V-like domain"

FT Modified-site 42 /note= "N-glycosylation site"

FT Modified-site 121 /note= "N-glycosylation site"

FT Region 139..157 /label= "Transmembrane region"

FT Region 158..190 /label= "Intracellular region"

XX WO200136630-A2.  
 XX 25-MAY-2001.  
 XX 15-NOV-2000; 2000WO-EP011697.  
 XX 15-NOV-1999; 99CA-02288307.  
 XX 15-NOV-1999; 99US-0040514.  
 XX (INNA-) INNATE PHARMA SAS.  
 XX (UYGE-) UNIV GENOVA.  
 XX Moretta A, Bottino C, Biassoni R;  
 XX WPI; 2001-329221/34.  
 XX N-PSDB; AAD06564.  
 XX Novel compound, useful for detection and/or quantifying the presence of  
 XX NK cells, comprises the amino acid sequences of the NKp30 molecule.  
 XX Claim 1; Fig 7B; 83pp; English.  
 XX The invention relates to human NKp30 receptor and its corresponding cDNA  
 XX molecule which is involved in natural cytotoxicity mediated by natural  
 XX killer (NK) cells and antibodies that identify the same. NKp30 receptor  
 XX is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively  
 XX expressed on the surface of human mature NK cells. NKp30 and its cDNA are  
 XX useful for detecting and/or quantifying the presence of NK cells in a  
 XX biological sample. The invention also provide kits for detecting and/or  
 XX quantifying the presence of NK cells, for the selective removal of NK  
 XX cells from a biological sample, for the positive and selective  
 XX stimulation of NK cell cytotoxicity. The invention further provides a  
 XX pharmaceutical composition which is used as a drug for grafting  
 XX enhancement, graft versus host (GvH) inhibition, stimulation of graft  
 XX versus tumour (GVT), and especially graft versus leukaemia (GvL), and for  
 XX the prevention, palliation and/or therapy of solid or liquid tumours,  
 XX such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
 XX microorganism, notably viral infection. NKp30 antibodies are useful for  
 XX identifying NKp30 natural ligands and allow assessment of the level of  
 XX surface NKp30 ligand expressed on an NK-susceptible target cell and the  
 XX comparison of this level to the standard physiological one. Hence NKp30  
 XX antibodies are useful in the diagnosis of tumours or of infection. The  
 XX present sequence is human NKp30 receptor  
 XX Sequence 190 AA;  
 XX Query Match 100.0%; Score 632; DB 4; Length 190;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LWVSQPPPIRTLESSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWVSQPPPIRTLESSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78  
 QY 61 PLASSRFLHDHQAEHLHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAEHLHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138  
 RESULT 6  
 ID ADO19810 standard; protein; 190 AA.  
 XX ADO19810;  
 XX ADO19810;  
 DT 12-AUG-2004 (first entry)  
 DE Human PRO polypeptide #367.  
 XX Human; PRO; immune related disorder; systemic lupus erythematosus;  
 XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;

KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;  
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;  
 KW diabetes mellitus; renal disease; demyelinating disease;  
 KW central nervous system; peripheral nervous system;  
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;  
 KW chronic inflammatory demyelinating polyneuropathy.  
 XX Homo sapiens.  
 OS WO2004043361-A2.  
 XX 27-MAY-2004.  
 XX 06-NOV-2003; 2003WO-US035268.  
 XX 08-NOV-2002; 2002US-0425235P.  
 XX (GETH ) GENENTECH INC.  
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;  
 XX Wood W, Wu TD;  
 XX WPI; 2004-420067/39.  
 XX N-PSDB; ADO19809.  
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
 XX treating an immune related disorder such as systemic lupus erythematosus,  
 XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
 XX spondyloarthritis.  
 XX Claim 7; SEQ ID NO 734; 1731pp; English.  
 XX The invention relates to human PRO polypeptides and the polynucleotides  
 XX encoding them. The polypeptides and polynucleotides are useful for  
 XX treating and diagnosing immune related disorders in mammals. The immune  
 XX related disorders include systemic lupus erythematosus, rheumatoid  
 XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 XX mellitus, immune-mediated renal disease, demyelinating diseases of the  
 XX central or peripheral nervous system, demyelinating polyneuropathy,  
 XX Guillain-Barre syndrome and chronic inflammatory demyelinating  
 XX polyneuropathy. This sequence represents a human PRO polypeptide of the  
 XX invention.  
 XX Sequence 190 AA;  
 XX Query Match 100.0%; Score 632; DB 8; Length 190;  
 XX Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
 XX Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LWVSQPPPIRTLESSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWVSQPPPIRTLESSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78  
 QY 61 PLASSRFLHDHQAEHLHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAEHLHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138  
 RESULT 7  
 ID ADO30923 standard; protein; 190 AA.  
 XX ADO30923;  
 XX ADO30923;  
 DT 23-SEP-2004 (first entry)  
 DE Human Nkp30 polypeptide.  
 XX Human Nkp30 polypeptide.  
 XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
FH 19..138  
FT /label= Extracellular region  
FT /note= "Region specifically described in Claim 3"  
FT 20..33  
FT Region  
FT /label  
FT /note= "Immunogenic peptide specifically described in Claim 3"  
FT 139..157  
FT Region  
FT /label= Transmembrane region  
FT /note= "Region specifically described in Claim 3"  
FT 158..190  
FT Region  
FT /label= Cytoplasmic tail  
FT /note= "Region specifically described in Claim 3"  
XX WO2004056392-A1.  
DN 08-JUL-2004.  
XX 22-DEC-2003; 2003WO-EP014716.  
XX 23-DEC-2002; 2002US-0435344P.  
PR (INNA-) INNATE PHARMA.  
XX Romagne F, Andre P;  
XX WPI; 2004-507595/48.  
DR Claim 3; SEQ ID NO 1; 35pp; English.  
XX  
CC The present sequence is that of human Nkp30, a 190 amino acid polypeptide (about 30 kDa on SDS-PAGE) that is selectively expressed by natural killer (NK) cells, and particularly by mature NK cells. Claimed pharmaceutical compositions that have a stimulating effect on the proliferation of NK cells comprise an antibody such as an anti-Nkp30 antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the antibody(ies) and cytokine(s) being administered together or separately to a subject. The anti-Nkp30 antibody is an isolated antibody or its antigen-binding fragment which specifically binds to Nkp30 or to a fragment ADQ30924-ADQ30927 of Nkp30. The pharmaceutical compositions, when used for daily subcutaneous injection, comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and lower than 1 million units/square meters/day of cytokine(s), are useful for the prevention, palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial prevention, palliation and therapy (claimed).  
XX  
SQ Sequence 190 AA;  
Query Match 100.0%; Score 632; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 3.6e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LWSQPPEIRTLGGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 19 LWSQPPEIRTLGGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78  
QY 61 PLASSRFLHQAEHLIRDVGRHDASIVYCRVEVLGVTGTGNTGLVWEKEHPQLGAGT 120  
DB 79 PLASSRFLHQAEHLIRDVGRHDASIVYCRVEVLGVTGTGNTGLVWEKEHPQLGAGT 138  
RESULT 8  
AAY06403

ID AAY06403 standard; protein; 201 AA.  
XX  
AC AAY06403;  
XX  
DT 20-SEP-1999 (first entry)  
XX  
DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX  
KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human; signal transduction; immunomodulator; antiinflammatory; autoimmune disease; inflammation; gene therapy; diagnosis.  
KW  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..12  
FT /note= "leader peptide"  
FT Protein 13..201  
FT /note= "mature protein"  
FT Modified-site 42  
FT /note= "N-glycosylated"  
FT Modified-site 68  
FT /note= "N-glycosylated"  
FT Modified-site 121  
FT /note= "N-glycosylated"  
FT Domain 139..162  
FT /note= "transmembrane domain"  
FT Peptide 166..201  
FT /note= "alternatively spliced C-terminal end"  
XX  
PN WO9923867-A2.  
XX  
PD 20-MAY-1999.  
XX  
XX 05-NOV-1998; 98WO-US023826.  
XX  
XX 07-NOV-1997; 97US-0064761P.  
XX (BIOJ ) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
DR N-PSDB; AAX59349.  
XX  
PT Novel B-cell myelin oligodendrocyte glycoproteins.  
XX  
PS Claim 2; Page 43; 43pp; English.  
XX  
CC This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory diseases. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)  
XX  
SQ Sequence 201 AA;  
Query Match 100.0%; Score 632; DB 2; Length 201;  
Best Local Similarity 100.0%; Pred. No. 3.9e-62;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LWSQPPEIRTLGGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
DB 19 LWSQPPEIRTLGGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTGLVVEKEHPQLGAGT 120  
 DB 79 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTGLVVEKEHPQLGAGT 138

RESULT 9  
 AAEL19109  
 ID AAEL19109 standard; protein; 135 AA.  
 AC AAEL19109;  
 DT 21-MAY-2002 (first entry)  
 DE Human NKp30 protein.  
 KW Human; natural killer cell activating protein; NKp46; therapy; virucide;  
 KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
 KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.  
 OS Homo sapiens.  
 XX WO200208287-A2.  
 XX 31-JAN-2002.  
 XX 19-JUL-2001; 2001WO-IL000664.  
 XX 20-JUL-2000; 2000IL-00137419.  
 XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX (UTNE ) UNIV BEN-GURION NEGEV.  
 XX Mandelboim O, Porgador A;  
 XX WPI; 2002-195870/25.  
 XX N-PSDB; AAD30466.  
 XX New targeting complex capable of targeting an active substance to a  
 XX target cell, comprising a target recognition segment and an active  
 XX segment, useful for treating pathologies associated with viral infections  
 XX or cancer.  
 XX Example 1; Page 108; 113pp; English.

XX The invention relates to compositions and methods for the treatment and  
 XX detection of a variety of viral infections, by using complex agents  
 XX comprising the natural killer (NK) cells activating proteins, NKp46 and  
 XX NKp44 and functional fragments thereof, linked to therapeutic or imaging  
 XX agents. The complex is useful for treating pathologies associated with  
 XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
 XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)  
 XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
 XX the imaging and monitoring of cancer. The complex may also be used to  
 XX detect the presence of abnormal cells in a sample. The antibodies can be  
 XX used to qualitatively or quantitatively detect the ligand for the  
 XX complex. The present sequence is human NKp30 protein  
 XX  
 XX Sequence 135 AA;

Query Match 97.6%; Score 617; DB 5; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-60;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTGLVVEKEHPQLG 117  
 DB 79 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTGLVVEKEHPQLG 135

RESULT 10  
 AAEL19110  
 ID AAEL19110 standard; protein; 369 AA.  
 AC AAEL19110;  
 DT 29-AUG-2003 (revised)  
 DT 21-MAY-2002 (first entry)  
 DE Human NKp30-IgG fusion protein.

XX Human; natural killer cell activating protein; NKp46; therapy; virucide;  
 XX viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
 XX detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;  
 XX immunoglobulin G; fusion protein.  
 XX Homo sapiens.  
 XX Chimeric.  
 XX  
 XX Key Location/Qualifiers  
 XX Region 1..135  
 XX /note= "Human NKp30"  
 XX Region 136..369  
 XX /note= "Human IgG"

XX WO200208287-A2.  
 XX 31-JAN-2002.  
 XX 19-JUL-2001; 2001WO-IL000664.  
 XX 20-JUL-2000; 2000IL-00137419.  
 XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
 XX (UTNE ) UNIV BEN-GURION NEGEV.  
 XX Mandelboim O, Porgador A;  
 XX WPI; 2002-195870/25.  
 XX N-PSDB; AAD30467.

XX New targeting complex capable of targeting an active substance to a  
 XX target cell, comprising a target recognition segment and an active  
 XX segment, useful for treating pathologies associated with viral infections  
 XX or cancer.  
 XX Example 1; Page 108-110; 113pp; English.  
 XX The invention relates to compositions and methods for the treatment and  
 XX detection of a variety of viral infections, by using complex agents  
 XX comprising the natural killer (NK) cells activating proteins, NKp46 and  
 XX NKp44 and functional fragments thereof, linked to therapeutic or imaging  
 XX agents. The complex is useful for treating pathologies associated with  
 XX viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
 XX -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)  
 XX and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
 XX the imaging and monitoring of cancer. The complex may also be used to  
 XX detect the presence of abnormal cells in a sample. The antibodies can be  
 XX used to qualitatively or quantitatively detect the ligand for the  
 XX complex. The present sequence is human NKp30- immunoglobulin G (IgG) Fc  
 XX region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 XX Sequence 369 AA;

Query Match 97.6%; Score 617; DB 5; Length 369;  
 Best Local Similarity 100.0%; Pred. No. 4e-60;  
 Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
 DB 19 LWSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHLDVRGHDASTYVCRVEVLGVGTGNGTGLVVEKEHPQLG 117



Db 79 PLASSRFLHDQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135  
 RESULT 11  
 ADP48750  
 ID ADP48750 standard; protein; 382 AA.  
 AC ADP48750;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human NKp30-Fc conjugate protein SEQ ID NO:12.  
 XX  
 KW polypeptide conjugate; target recognition; natural killer cell receptor;  
 KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;  
 KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;  
 KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;  
 KW human; natural killer cytotoxicity receptor conjugate;  
 KW NKp30-Fc conjugate.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..25  
 FT Protein /label= signal  
 FT FT 26..382  
 FT /note= "NKp30-Fc conjugate"  
 FT FT 26..31  
 FT /note= "KpnI site"  
 FT Region 32..148  
 FT /label= NKp30  
 FT Region 149..382  
 FT /label= Fc  
 XX  
 PN WO2004053054-A2.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 09-DEC-2003; 2003WO-IL001040.  
 XX  
 PR 09-DEC-2002; 2002US-0431728P.  
 XX  
 PA (NATS-) NATSPEARS LTD.  
 XX  
 PI Mandelboim O, Porgador A;  
 XX  
 DR WPI; 2004-468830/44.  
 DR N-PSDB; ADP48757.  
 XX  
 PT New polypeptide conjugate comprising a target recognition segment  
 PT comprising a Natural Killer cell receptor consisting of NKp30, useful in  
 PT preparing a composition for treating a neoplastic disease.

XX Claim 5; SEQ ID NO 4; 66pp; English.  
 XX  
 XX The present invention describes a polypeptide conjugate comprising: (a) a  
 CC target recognition segment comprising a natural killer cell receptor  
 CC (NCR) or its fragment consisting of NKp30 or its fragment that binds to a  
 CC cellular ligand expressed on the surface of a target tumour cell; and (b)  
 CC a second segment comprising an active agent capable of exerting a  
 CC cytotoxic effect on the target cell. Also described: (1) an isolated  
 CC polynucleotide encoding the polypeptide conjugate; (2) a vector  
 CC comprising the polynucleotide; (3) a host cell comprising the vector and  
 CC capable of expressing the polypeptide conjugate; (4) a pharmaceutical  
 CC composition comprising the polypeptide conjugate and a carrier,  
 CC stabiliser or diluent; (5) treating a neoplastic disease in a subject;  
 CC (6) inhibiting the growth of a tumour in a subject; and (7) delivering a  
 CC cytotoxic substance to a target tumour cell in a subject. The polypeptide  
 CC conjugate has cytostatic activity, and can be used in gene therapy. The  
 CC polypeptide conjugate is useful in preparing a composition for treating a  
 CC neoplastic disease associated with a solid tumour or a non-solid tumour,  
 CC e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell

CC carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell  
 CC lymphoma or leukaemia. The present sequence represents a human natural  
 CC killer cytotoxicity receptor conjugate, designated NKp30-Fc conjugate,  
 CC which is used in the exemplification of the present invention.

XX SQ Sequence 382 AA;

Query Match 96.0%; Score 607; DB 8; Length 382;  
 Best Local Similarity 99.1%; Pred. No. 5.5e-59;  
 Matches 116; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLLEGSSAFPCSFNASQGRLAIGSVTWFDRDEVVPCKEVRNGTPEFRGLA 60  
 Db 32 LWSQPPEIRTLLEGSSAFPCSFNASQGRLAIGSVTWFDRDEVVPCKEVRNGTPEFRGLA 91  
 QY 61 PLASSRFLHDQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 117  
 Db 92 PLASSRFLHDQAEHLHIRDVGRGHDSIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 148

# RESULT 12

AAU75565  
 ID AAU75565 standard; protein; 139 AA.

XX  
 AC AAU75565;

DT 23-APR-2002 (first entry)

XX Murine T cell receptor beta chain.

XX  
 KW Immunoglobulin superfamily; GP286; human; immunosuppressive;  
 KW autoimmune disease; rheumatoid arthritis; cancer; multiple sclerosis;  
 KW acquired immune deficiency syndrome; AIDS; inflammatory disorder;  
 KW pancreatic; antirheumatic; antipsoriatic; dermatological; antianaemic;  
 KW cytostatic; antileukaemic; antiasthmatic; antiallergic;  
 KW T cell receptor beta chain.

XX Mus sp.

XX WO200200727-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US020039.

XX 23-JUN-2000; 2000US-0213630P.

PR 13-APR-2001; 2001US-0283813P.

XX (BIOJ) BIOGEN INC.

XX Carulli JP, Lukashin AV, Kilburn DR, Mathur P;

DR WPI; 2002-090520/12.

XX Isolated polynucleotide encoding a novel human immunoglobulin superfamily  
 PT member, named GP286, useful in the treatment of a disease condition that  
 PT relates to the immune system, e.g. a transplantation disorder or an  
 PT autoimmune disease.

PS Disclosure; Page 167; 180pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel  
 CC human immunoglobulin superfamily member, named GP286. The GP286  
 CC polynucleotide and polypeptide are useful for the treatment of a disease  
 CC condition that relates to the immune system, preferably a disease  
 CC condition that relates to T cells, e.g. a transplantation disorder, an  
 CC autoimmune disease (e.g. rheumatoid arthritis, systemic lupus  
 CC erythematosus, psoriasis, Sjogren's Syndrome, thyroiditis, Graves'  
 CC disease, pulmonary fibrosis, bronchiolitis obliterans, haemolytic anaemia  
 CC or Wegener's granulomatosis), cancer (e.g. leukaemia or lymphoma),  
 CC multiple sclerosis, graft versus host disease, Kawasaki syndrome,  
 CC acquired immune deficiency syndrome (e.g. AIDS) or an inflammatory  
 CC disorder (e.g. asthma, allergies, adult respiratory distress syndrome and

CC acute pancreatitis or chronic pancreatitis). The gp286 nucleic acids can  
 CC be used as probes for detecting, characterising and quantifying gp286  
 CC nucleic acids. The present sequence represents the amino acid sequence of  
 CC murine T cell receptor beta chain used in the method of the invention  
 XX  
 SQ Sequence 139 AA;

Query Match 18.8%; Score 118.5; DB 5; Length 139;  
 Best Local Similarity 30.2%; Pred. No. 5.8e-05;  
 Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;  
 QY 2 WVS-----PPERTLEGSSAFPCSFNASQGLAIGSVTWPERDE-----VWPG 45  
 DB 18 WVSQGVKQSPSALSLQEGTSSALRCNFS-----IATTVQWFLQNSRSLMNLFLVLP- 71  
 QY 46 KEVNGTPEFRGLRIAPLASSRFLHDHQAELHIRDVRGHDAIYVCRVEVLGLG--VGTGN 103  
 DB 72 ----GTYE-NGLKSTFNSK---ESYSTLHIRDAQLEDGSGTYFCAAEVEGTGSKLSFGK 122  
 QY 104 GTRLVVEKE 112  
 DB 123 GAKLTVSPD 131

RESULT 13  
 AAM24182  
 ID AAM24182 standard; protein; 138 AA.  
 XX  
 AC AAM24182;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX  
 DE Rhesus monkey EST encoded protein SEQ ID NO: 1707.  
 XX  
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;  
 KW gene therapy; nutrition.  
 XX  
 OS Macaca mulatta.  
 XX  
 EN WO200154477-A2.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US002687.  
 XX  
 XX 25-JAN-2000; 2000US-00491404.  
 PR 17-JUL-2000; 2000US-00617746.  
 PR 03-AUG-2000; 2000US-00631451.  
 PR 15-SEP-2000; 2000US-00663870.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 XX WPI; 2001-476164/51.  
 DR N-PSDB; AAM98841.  
 XX  
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use.  
 XX  
 XX Claim 20; Page 1137-1138; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
 XX proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a  
 CC protein of the invention

XX Sequence 138 AA;  
 SQ  
 Query Match 16.7%; Score 105.5; DB 4; Length 138;  
 Best Local Similarity 29.1%; Pred. No. 0.0016;  
 Matches 37; Conservative 19; Mismatches 46; Indels 25; Gaps 6;  
 QY 3 VSQPE-IRTLGSSAFPCSFNASQGLAIGSVTWPERDEVVPCKEVNRGTPPERGLAP 61  
 DB 22 VTQSPALRLQEGESSLNCSTYVS-----GLRGLFWYRQD--PGK-----GPEFLFTLYS 70  
 QY 62 LASSR-----FLHDHQAELHIRDVRGHDAIYVCRVEVL-----GLGVGTGNGTRLV 108  
 DB 71 AGEKEKERLKAATLTKKESFLHITAPKPEDSATILCAVQAFHSGGGADGLTFKGIRLK 130  
 QY 109 VEKEHPQ 115  
 DB 131 VLALYPE 137

RESULT 14  
 AAB68882  
 ID AAB68882 standard; protein; 140 AA.  
 XX  
 AC AAB68882;  
 XX  
 DT 24-APR-2001 (first entry)  
 XX  
 DE Human RECAP polypeptide, SEQ ID NO: 12.  
 XX  
 KW Human; RECAP; receptors and associated proteins; cerebroprotective;  
 KW neotropic; neuroprotective; anticonvulsant; antiparkinsonian; anti-HIV;  
 KW antidiabetic; immunosuppressant; immunomodulator; antiinflammatory;  
 KW antithyroid; immunosuppressive; nephrotropic; antigout; thyromimetic;  
 KW cytostatic; antibacterial; vitucide; fungicide; protozoacide;  
 KW antiarteriosclerotic; hepatotropic; gene therapy; infection; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200107612-A2.  
 XX  
 PD 01-FEB-2001.  
 XX  
 XX 21-JUL-2000; 2000WO-US020035.  
 XX  
 XX 21-JUL-1999; 99US-0145232P.  
 PR 07-OCT-1999; 99US-0158578P.  
 PR 12-NOV-1999; 99US-0165192P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Au-Young J, Bandman O, Tang YT, Yue H, Azimzai Y, Burford N;  
 PI Baughn MR, Lu DAM, Hillman JL, Patterson C, Lal P;  
 XX  
 XX WPI; 2001-168554/17.  
 DR N-PSDB; AAF58606.  
 XX  
 XX Novel receptors and associated proteins for diagnosis and treatment of  
 PT neurological disorders, immunological disorders including autoimmune/  
 PT inflammatory disorders and cell proliferative disorders such as cancer.  
 XX  
 XX Claim 1; Page 104; 128pp; English.

XX The present sequence is a human RECAP (receptors and associated proteins)  
 CC polypeptide. RECAP polynucleotides and polypeptides are useful in the  
 CC diagnosis, treatment and prevention of neurological disorders such as  
 CC stroke, Alzheimer's disease, Pick's disease, Huntington's disease,  
 CC dementia, Parkinson's disease, Down's syndrome, amyotrophic lateral  
 CC sclerosis, multiple sclerosis, bacterial and viral meningitis, CJD  
 CC (Creutzfeldt-Jakob disease), GSS (Gerstmann-Strausler-Scheinker  
 CC syndrome); immunological disorders, including autoimmune/inflammatory  
 CC disorders such as AIDS, DiGeorge's syndrome, severe combined  
 CC immunodeficiency disease (SCID), Chediak-Higashi syndrome, Cushing's

CC disease, Addison's disease, autoimmune thyroiditis, Crohn's disease,  
CC diabetes mellitus, Good pasture's syndrome, gout, Grave's diseases,  
CC Hashimoto's thyroiditis, Sjogren's syndrome, Werner's syndrome, viral,  
CC bacterial, fungal, parasitic, protozoal, and helminthic infections; and  
CC cell proliferation disorders such as arteriosclerosis, atherosclerosis,  
CC cirrhosis, hepatitis and cancer  
XX  
SQ Sequence 140 AA;  
Query Match 16.6%; Score 105; DB 4; Length 140;  
Best Local Similarity 30.3%; Pred. No. 0.0019;  
Matches 36; Conservative 20; Mismatches 37; Indels 26; Gaps 7;  
Qy 3 VSQPE-IRTEGSAFLPCSFNASQGRLAIGSVTWFRDEWPGKEVRNGTPEFRGLAP 61  
Db 25 VTQSPALRLQEGESSLNCSTVVS----GLRGLFWYRQD--PGK-----GPFFLTLLYS 73  
Qy 62 LASR-----FLHDQALHLDVRGHDASIVYCRVEVLGVGT----GNGTLLV 109  
Db 74 AGEKEKERLKATLTKEKSFHTAPKPEDSASYLCAVQG---GIGNVLHCGSGTQVW 129  
RESULT 15  
RAR97726  
ID AAR97726 standard; protein; 262 AA.  
XX  
AC AAR97726;  
XX  
DT 18-SEP-1996 (first entry)  
XX  
DE B10 single chain T-cell receptor.  
XX  
KW Single chain T-cell receptor; TCR; maltose binding protein;  
KW MBP-B10 scTCR; fusion protein; V-alpha; V-beta; antibody; vaccine;  
KW cytochrome-c.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Cleavage-site 6..7 /note= "thrombin cleavage site"  
FT Domain 7..123 /label= V-beta  
FT /note= "residue 8 (Pro in the wild-type) is substituted  
FT by Ser to facilitate thrombin cleavage"  
FT Region 124..150 /label= Linker  
FT Domain 151..256 /label= V-alpha  
FT Domain 257..262 /label= Hexahistidine\_tail  
XX  
FN WO9613593-A2.  
XX  
XX  
PD 09-MAY-1996.  
XX  
PF 26-OCT-1995; 95WO-US013770.  
XX  
PR 26-OCT-1994; 94US-00329310.  
PR 01-DEC-1994; 94US-00347893.  
PR 06-JUN-1995; 95US-00468131.  
XX  
XX (PROC-) PROCEPT INC.  
XX  
XX Banerji J, Khandekar S, Bettencourt B, Naylor J, Jones B;  
PI McKeever U, Jesson M, Dwyer D;  
XX  
DR WPI; 1996-239502/24.  
DR N-PSDB; AAT29758.  
XX  
XX New fusion proteins comprising a single chain T-cell receptor - used to  
PT develop prods. for use in detection, diagnosis, functional studies and  
PT therapy involving immune responses.

XX  
PS Example 1; Page 64-65; 104pp; English.  
XX  
CC A soluble single chain T-cell receptor (scTCR) (AAR97726) comprises the V  
CC -beta region of cytochrome c-specific B10 T-cell receptor joined to the  
CC D10 V-alpha region via a linker peptide. It is obt'd. by PCR amplification  
CC of V-beta and V-alpha sequences, and cloning into a vector that encodes  
CC the linker. The entire scTCR sequence (AAT29758) is then cloned into  
CC vector pPR998 which encodes maltose binding protein (MBP). The MBP-B10  
CC scTCR fusion protein is expressed in E. coli and purified by affinity  
CC chromatography. Thrombin cleavage yields a soluble scTCR useful in  
CC detection, diagnosis, functional studies and therapy involving immune  
CC responses  
XX  
SQ Sequence 262 AA;  
Query Match 16.5%; Score 104; DB 2; Length 262;  
Best Local Similarity 30.5%; Pred. No. 0.0054;  
Matches 36; Conservative 17; Mismatches 49; Indels 16; Gaps 6;  
Qy 3 VSQPEIETL-EGSSAFLPCSFNASQGRLAIGSVTWTF---RDEVVPGKEVRNGTPEFRG 57  
Db 151 VEQSPSALSLEHGTDLSALRCNFTTT----MRAVQWFRKNSRGSILNLFYLSGTKE-NG 204  
Qy 58 RLAPLASSRFLHDQALHLDVRGHDASIVYCRVEVLGLG--VGTGNGTLLVVEKEH 113  
Db 205 RLKSAFDSK---ERYSTLHIDRQEDSGTYFCAAEATSGQKLVFGQGTILKVYHHH 259  
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Job time : 130.639 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 107.268 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-4  
Perfect score: 632  
Sequence: 1 LWSVQPPRTLEGSSAFIP.....TGNGRLVVEKEHPQLGAGT 120

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues  
Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	632	100.0	120	13	US-10-036-444-4
2	632	100.0	170	16	US-10-036-259-5
3	632	100.0	190	13	US-10-036-444-2
4	632	100.0	200	16	US-10-036-259-4
5	632	100.0	201	16	US-10-036-259-6
6	617.5	97.7	161	16	US-10-036-259-10
7	617.5	97.6	135	15	US-10-333-481-17
8	617.5	97.5	369	15	US-10-333-481-18
9	603	95.4	175	16	US-10-036-259-8
10	603	95.4	185	16	US-10-036-259-7
11	603	95.4	198	16	US-10-036-259-9
12	118.5	18.8	139	14	US-10-312-495-6
13	107	16.9	1814	16	US-10-367-094-162

14	103	16.3	136	15	US-10-276-774-1657	Sequence 1657, Ap
15	103	16.3	329	14	US-10-104-047-3709	Sequence 3709, Ap
16	103	16.3	3931	14	US-10-120-801-18	Sequence 18, Appl
17	102	16.1	3409	16	US-10-367-094-165	Sequence 165, Appl
18	99	15.7	246	10	US-09-909-567B-49	Sequence 49, Appl
19	98.5	15.6	252	10	US-09-880-748-1495	Sequence 1495, Ap
20	98.5	15.6	252	14	US-10-233-418-1495	Sequence 1495, Ap
21	96.5	15.3	125	16	US-10-432-006-2	Sequence 2, Appl
22	95.5	15.1	218	13	US-10-032-045-1	Sequence 1, Appl
23	94.5	15.0	175	16	US-10-696-259-13	Sequence 13, Appl
24	94	14.9	526	9	US-09-910-174A-9	Sequence 9, Appl
25	94	14.9	526	9	US-09-955-866-13	Sequence 13, Appl
26	94	14.9	526	9	US-09-896-738-19	Sequence 19, Appl
27	94	14.9	526	14	US-10-156-424A-7	Sequence 7, Appl
28	94	14.9	526	16	US-10-408-765A-1673	Sequence 1673, Ap
29	94	14.9	526	16	US-10-644-671-9	Sequence 9, Appl
30	93	14.7	1598	10	US-09-863-776-59	Sequence 59, Appl
31	93	14.7	1694	10	US-09-863-776-57	Sequence 57, Appl
32	92.5	14.6	388	15	US-10-362-591-4	Sequence 4, Appl
33	91.5	14.5	223	16	US-10-790-386-42	Sequence 42, Appl
34	91	14.4	205	9	US-08-252-150-9	Sequence 9, Appl
35	91	14.4	253	10	US-09-880-748-1545	Sequence 1545, Ap
36	91	14.4	253	14	US-10-293-418-1545	Sequence 1545, Ap
37	90.5	14.3	502	14	US-10-363-427-24	Sequence 24, Appl
38	90	14.2	524	15	US-10-042-865-67	Sequence 67, Appl
39	89.5	14.2	110	14	US-10-269-805-50	Sequence 50, Appl
40	89.5	14.2	175	16	US-10-696-259-12	Sequence 12, Appl
41	89.5	14.2	383	10	US-09-898-195A-11	Sequence 11, Appl
42	89.5	14.2	383	14	US-10-057-288-6	Sequence 6, Appl
43	89.5	14.2	383	14	US-10-155-514-10	Sequence 10, Appl
44	89.5	14.2	383	15	US-10-419-008-11	Sequence 11, Appl
45	89	14.1	124	16	US-10-696-259-16	Sequence 16, Appl

## ALIGNMENTS

## RESULT 1

US-10-036-444-4  
; Sequence 4, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1660  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-4

Query Match 100.0%; Score 632; DB 13; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.2e-61;  
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LWSVQPPRTLEGSSAFIPCSFNASQGRLAIGSVTFWRDEVPKGVNQTPEFRGLA 60  
Db 1 LWSVQPPRTLEGSSAFIPCSFNASQGRLAIGSVTFWRDEVPKGVNQTPEFRGLA 60  
QY 61 PLASSRFLHDHQAELHIRDVEGHDAIYVCRVVLGVGTGNGTRLVVEKEHPQLGAGT 120  
Db 61 PLASSRFLHDHQAELHIRDVEGHDAIYVCRVVLGVGTGNGTRLVVEKEHPQLGAGT 120

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19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 78
61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

RESULT 4
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match 100.0%; Score 632; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

RESULT 5
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match 100.0%; Score 632; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138

RESULT 3
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; APPLICANT: UNIVERSITA DI GENOVA
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match 100.0%; Score 632; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 5.7e-61;
Matches 120; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEWVPGKEVRNGTPEFRGLA 78
QY 61 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 79 PLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 138
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Query Match 100.0%; Score 632; DB 16; Length 201;  
Best Local Similarity 100.0%; Pred. No. 6.1e-61; Indels 0; Gaps 0;  
Matches 120; Conservative 0; Mismatches 0;

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Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGACT 120  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGACT 138

RESULT 6  
US-10-696-259-10  
; Sequence 10, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-696-259-10

Query Match 97.7%; Score 617.5; DB 16; Length 161;  
Best Local Similarity 99.2%; Pred. No. 1.8e-59; Indels 1; Gaps 1;  
Matches 119; Conservative 0; Mismatches 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGACT 120  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGACT 137

RESULT 7  
US-10-333-481-17  
; Sequence 17, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Offer Mandelboim  
; APPLICANT: Angel Porgador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 135  
; TYPE: PRT  
; ORGANISM: homo sapiens

US-10-333-481-17  
Query Match 97.6%; Score 617; DB 15; Length 135;  
Best Local Similarity 100.0%; Pred. No. 1.6e-59; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 117  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135

RESULT 8  
US-10-333-481-18  
; Sequence 18, Application US/10333481  
; Publication No. US20040072256A1  
; GENERAL INFORMATION:  
; APPLICANT: Offer Mandelboim  
; APPLICANT: Angel Porgador  
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC  
; FILE REFERENCE: 68657  
; CURRENT APPLICATION NUMBER: US/10/333,481  
; CURRENT FILING DATE: 2003-08-04  
; PRIOR APPLICATION NUMBER: PCT/IL01/00664  
; PRIOR FILING DATE: 2001-07-19  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 369  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-333-481-18

Query Match 97.6%; Score 617; DB 15; Length 369;  
Best Local Similarity 100.0%; Pred. No. 5.7e-59; Indels 0; Gaps 0;  
Matches 117; Conservative 0; Mismatches 0;

Qy 1 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60  
Db 19 LWSQPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 78

Qy 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 117  
Db 79 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135

RESULT 9  
US-10-696-259-8  
; Sequence 8, Application US/10696259  
; Publication No. US20040110218A1  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 175  
; TYPE: PRT

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; ORGANISM: Homo sapien
US-10-696-259-8

Query Match          95.4%; Score 603; DB 16; Length 175;
Best Local Similarity 98.3%; Pred. No. 7.8e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 10
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BNOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match          95.4%; Score 603; DB 16; Length 185;
Best Local Similarity 98.3%; Pred. No. 8.3e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 11
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BNOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05

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; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match          95.4%; Score 603; DB 16; Length 198;
Best Local Similarity 98.3%; Pred. No. 9e-58;
Matches 118; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 LWSQPPEIRLTGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 60
DB 19 LWSQPPEIRT-EGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLA 77

QY 61 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTGNGTRLVVEKEHPQLGAGT 120
DB 78 PLASSRFLHDHQAELHIRDVRGHDASIYVCRVE-LGLGVGTGNGTRLVVEKEHPQLGAGT 136

RESULT 12
US-10-312-495-6
; Sequence 6, Application US/10312495
; Publication No. US20030165495A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: A099PCT000454-124
; CURRENT APPLICATION NUMBER: US/10/312,495
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/213,630
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/283,813
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-312-495-6

Query Match          18.8%; Score 118.5; DB 14; Length 139;
Best Local Similarity 30.2%; Pred. No. 7.4e-05;
Matches 39; Conservative 17; Mismatches 40; Indels 33; Gaps 7;

QY 2 WVS-----QPPEIRTLGSSAFPCSFNASQGRLAIGSVTWFRDE-----VVPG 45
DB 18 WVSQDVQKQSPSALSQEGTSSALRCNFS-----IATTVQWFLQNSRGLMNLFLVLP- 71

QY 46 KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLG--VGTGN 103
DB 72 -----GTKE-NGRLKSTFNK---ESYSTLHIRDQAQDSGTFCFAEVEGTGSKLSFGK 122

QY 104 GTRLVVEKE 112
DB 123 GAKLTVSPD 131

RESULT 13
US-10-367-094-162
; Sequence 162, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: S29452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14

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; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 1814
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-367-094-162

Query Match      16.3%; Score 107; DB 16; Length 1814;
Best Local Similarity 28.7%; Pred. No. 0.032;
Matches 25; Conservative 12; Mismatches 30; Indels 20; Gaps 2;

QY 7 PEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 818 PDLSTIEGSHALPCTAKGSP-----PAITWCKD-----GHLVSGAECK 857

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVRE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 858 FTIQPSGELLVKNSEGQDAGTYTCTAE 884

RESULT 14
US-10-276-774-1657
; Sequence 1657, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1657
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-1657

Query Match      16.3%; Score 103; DB 15; Length 136;
Best Local Similarity 28.7%; Pred. No. 0.0036;
Matches 25; Conservative 11; Mismatches 31; Indels 20; Gaps 2;

QY 7 PEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 32 PDLSTIEGSHALPCKARGSP-----PNITWCKD-----GQPVSGAECK 71

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVRE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 FTIQPSGELLVKNLEGQDAGTYTCTAE 98

RESULT 15
US-10-104-047-3709
; Sequence 3709, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3709
; LENGTH: 329
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3709

Query Match      16.3%; Score 103; DB 14; Length 329;
Best Local Similarity 28.7%; Pred. No. 0.011;
Matches 25; Conservative 11; Mismatches 31; Indels 20; Gaps 2;

QY 7 PEIRTEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLAPLASSR 66
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 PDLSTIEGSHALPCKARGSP-----PNITWCKD-----GQPVSGAECK 215

QY 67 FLHDHQAEHLHIRDVRGHDASIYVCVRE 93
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 FTIQPSGELLVKNLEGQDAGTYTCTAE 242

Search completed: November 16, 2004, 19:45:04
Job time : 108.268 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 33.7401 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-4

Perfect score: 632

Sequence: 1 LKWSQPEIRTEGSAFLP.....TNGTRLVVEKHPQLGACT 120

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*
- 4: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*
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- 6: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	101.5	16.1	267	1	US-08-416-336-2
2	99	15.7	270	3	US-09-082-593-10
3	95.5	15.1	218	4	US-10-026-045-1
4	94	14.9	526	4	US-09-910-174B-9
5	94	14.9	526	4	US-09-620-461-9
6	94	14.9	526	4	US-08-724-394A-1
7	92	14.6	174	3	US-08-804-180C-4
8	89.5	14.2	120	3	US-09-171-945-89
9	89.5	14.2	137	3	US-08-804-180C-2
10	89.5	14.2	331	5	PCT-US95-15696-2
11	88	13.9	226	4	US-09-311-784A-32
12	88	13.9	946	5	PCT-US95-08493-13
13	87.5	13.8	120	4	US-09-472-087-102
14	87.5	13.8	187	1	US-08-667-684-14
15	87.5	13.8	187	1	US-08-008-898-14
16	87.5	13.8	187	2	US-08-459-818-14
17	87.5	13.8	187	2	US-08-889-666-14
18	87.5	13.8	187	2	US-08-465-078-14
19	87.5	13.8	187	2	US-08-725-776-14
20	87.5	13.8	187	2	US-08-488-062-14
21	87.5	13.8	187	3	US-08-328-208A-14
22	87.5	13.8	187	4	PCT-US95-06726-36
23	87.5	13.8	187	5	US-10-026-045-1
24	87.5	13.8	218	4	US-08-328-208A-17
25	87.5	13.8	223	3	PCT-US94-10257A-2
26	87.5	13.8	247	5	US-09-472-087-100
27	87.5	13.8	364	4	US-09-472-087-100

Sequence 26, Appl  
Sequence 28, Appl  
Sequence 26, Appl  
Sequence 28, Appl  
Sequence 24, Appl  
Sequence 24, Appl  
Sequence 2, Appl  
Sequence 17, Appl  
Sequence 81, Appl  
Sequence 10, Appl  
Sequence 20, Appl  
Sequence 20, Appl  
Sequence 213, App  
Sequence 213, App  
Sequence 213, App  
Sequence 213, App  
Sequence 79, Appl

ALIGNMENTS

RESULT 1  
US-08-416-336-2  
; Sequence 2, Application US/08416336  
; Patent No. 5807714  
; GENERAL INFORMATION:  
; APPLICANT: Ishizaka, Kimishige  
; APPLICANT: Ishii, Yasuyuki  
; TITLE OF INVENTION: METHOD OF PRODUCTION OF ANTIGEN-SPECIFIC  
; TITLE OF INVENTION: GLYCOSYLATION INHIBITING FACTOR  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/416,336  
; FILING DATE: 04-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa H.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07246/010001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-416-336-2

Query Match  
Best Local Similarity 16.1%; Score 101.5; DB 1; Length 267;  
Matches 38; Conservative 16; Mismatches 39; Indels 33; Gaps 8;  
QY 2 WVS-----QPPEIRTEGSAFLPCTSNAGKATGCVTFWDEVPVGEVKN-----50  
Db 18 WVSQKVKQSPSALSQEGTNSALRCNFS-----IAATTQWFLQN--PRGSLMNLFLYV 70  
QY 51 -GTPEFRGRGLAPLASSRFLHDHQAELHRLDVRGHDASIVYVCVVEVLGLGVGT-----GN 103

Db 71 PGTK-NGRLKSTFNSK---ESYTLHIRDAQEDSGTYFCAAE-----GGGSKYLTFGK 122  
QY 104 GTRLVV 109  
Db 123 GTLLTV 128

RESULT 2  
US-09-082-593-10  
; Sequence 10, Application US/09082593  
; Patent No. 6180104  
; GENERAL INFORMATION:  
; APPLICANT: DAVIS, MARK M.  
; APPLICANT: HEDRICK, STEPHEN M.  
; TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT  
; FILE REFERENCE: JX1193-195DIV2  
; CURRENT APPLICATION NUMBER: US/09/082,593  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 10  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-082-593-10

Query Match 15.7%; Score 99; DB 3; Length 270;  
Best Local Similarity 29.4%; Pred. No. 0.0023;  
Matches 37; Conservative 17; Mismatches 42; Indels 30; Gaps 8;

QY 3 VSOPPE-IRTEGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGKEVR-----NGTPE 54  
Db 24 VQSPESLIPEGARTSLNCTFSDSASQY-----FWYRQH--SGKAPKALMSIFNSGEKE 77  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVCVRVEVLGIGVGTGNTGLRVVVEKEHP 114  
Db 78 -EGRFTHLNKASLH---FSLHIRDSQPSDSALYLCAVTLYG-----GSGNKLI----- 122  
QY 115 QLGA GT 120  
Db 123 -FGTGT 127

RESULT 3  
US-10-026-045-1  
; Sequence 1, Application US/10026045  
; Patent No. 6573236  
; GENERAL INFORMATION:  
; APPLICANT: Genain, Claude P  
; APPLICANT: Hauser, Stephen L  
; TITLE OF INVENTION: Inhibiting MOG-Antibody Binding  
; FILE REFERENCE: UCSF99-020-3  
; CURRENT APPLICATION NUMBER: US/10/026,045  
; CURRENT FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 09/384,036  
; PRIOR FILING DATE: 1999-08-26  
; PRIOR APPLICATION NUMBER: us 60/097,953  
; PRIOR FILING DATE: 1998-08-26  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 1  
; LENGTH: 218  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-10-026-045-1

Query Match 15.1%; Score 95.5; DB 4; Length 218;  
Best Local Similarity 36.2%; Pred. No. 0.0045;  
Matches 34; Conservative 8; Mismatches 33; Indels 19; Gaps 6;

QY 9 IRTLEGSAFLPCSFNASQGRLAIG-SVTWFRDEVVPGKEV-----RNG-----TPBFR 56

Db 12 ITRALVGEAEALPC--RISPGKNATGMVEVGYRS---PFSRVVHLYRNGKQDQAEQAPEYR 66  
QY 57 GRPLAPLASSRFLHDHQAELHIRDVGRGHDAIYVC 90  
Db 67 GRTELLKES--IGEGKVALRIQNVRFPSDEGGYTC 98

RESULT 4  
US-09-910-174B-9  
; Sequence 9, Application US/09910174B  
; Patent No. 6630575  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6630575el Members of the B7  
; FILE REFERENCE: 35800/236924  
; CURRENT APPLICATION NUMBER: US/09/910,174B  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 09/620,461  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-910-174B-9

Query Match 14.9%; Score 94; DB 4; Length 526;  
Best Local Similarity 39.6%; Pred. No. 0.021;  
Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-IRTEGSAFLPC--SFNASQGRLAIGSVTWFRDEVVPGKEV-RNG-----TPE 54  
Db 34 PPEPILAVVGDEALPCRLSPNASAEHL---ELRWFRKKVSPAVLVHRDGRGEAEQMP 90  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVC 90  
Db 91 YRGR-ATLVQDGIAGRVA-LRINGVRVSDGGEYTC 124

RESULT 5  
US-09-620-461-9  
; Sequence 9, Application US/09620461  
; Patent No. 6635750  
; GENERAL INFORMATION:  
; APPLICANT: Coyle, Anthony J.  
; APPLICANT: Fraser, Christopher C.  
; APPLICANT: Manning, Stephen  
; TITLE OF INVENTION: B7-H2 Molecules, No. 6635750el Members of the B7  
; FILE REFERENCE: 5800-149  
; CURRENT APPLICATION NUMBER: US/09/620,461  
; CURRENT FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 526  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-620-461-9

Query Match 14.9%; Score 94; DB 4; Length 526;  
Best Local Similarity 39.6%; Pred. No. 0.021;  
Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-IRTEGSAFLPC--SFNASQGRLAIGSVTWFRDEVVPGKEV-RNG-----TPE 54  
Db 34 PPEPILAVVGDEALPCRLSPNASAEHL---ELRWFRKKVSPAVLVHRDGRGEAEQMP 90  
QY 55 FRGLAPLASSRFLHDHQAELHIRDVGRGHDAIYVC 90

Db 91 YRGR-ATLVQDGIAGRVA-LRIRGVRSDDGEYTC 124

## RESULT 6

US-08-724-394A-1  
; Sequence 1, Application US/08724394A  
; Patent No. 5872237  
; GENERAL INFORMATION:  
; APPLICANT: Feder, John N.  
; APPLICANT: Kronmal, Gregory S.  
; APPLICANT: Lauer, Peter M.  
; APPLICANT: Ruddy, David A.  
; APPLICANT: Thomas, Winston  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el  
; TITLE OF INVENTION: Sequences and Antibodies Thereto  
; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA

; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/724,394A  
; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 01957-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 589 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: peptide  
; FEATURE:  
; NAME/KEY: Region  
; LOCATION: 1-589  
; OTHER INFORMATION: /note= "BT"

US-08-724-394A-1

Query Match 14.9%; Score 94; DB 2; Length 589;  
Best Local Similarity 39.6%; Pred. No. 0.025;  
Matches 38; Conservative 5; Mismatches 37; Indels 16; Gaps 7;

QY 6 PPE-INTLEGSSAFIPC-SFNASQGRLAIGSVTWFRDEVPCKEV-RNG-----TPE 54  
Db 37 PPEPILAVVGEDAEPLCPSPNASAEHL---ELRWFKKVSAPVLVRDGRQEAEQMPPE 93

QY 55 FRGRAPLASSRFLHDHQAELHIRDVGRHDSIYVC 90  
Db 94 YRGR-ATLVQDGIAGRVA-LRIRGVRSDDGEYTC 127

## RESULT 7

US-08-804-180C-4  
; Sequence 4, Application US/08804180C  
; Patent No. 6107056  
; GENERAL INFORMATION:

; APPLICANT: Martin K. Oaks  
; TITLE OF INVENTION: scTLA-4 and Its Soluble Products  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Thomas M. Wozny

; STREET: 100 East Wisconsin Avenue  
; CITY: Milwaukee  
; STATE: Wisconsin  
; COUNTRY: USA  
; ZIP: 53202

; COMEUTER READABLE FORM:  
; MEDIUM TYPE: 3.50 inch Disk  
; COMPUTER: IBM  
; OPERATING SYSTEM: DOS  
; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,180C  
; FILING DATE: February 20, 1997  
; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:  
; NAME: Thomas M. Wozny  
; REGISTRATION NUMBER: 28,922  
; REFERENCE/DOCKET NUMBER: 3284-00003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 271-7590  
; TELEFAX: (414) 271-5770

; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 174  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: Polypeptide  
; DESCRIPTION: Internal fragment  
; HYPOTHETICAL: no  
; FRAGMENT TYPE: Internal fragment  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus No. 6107056vegicus

; STRAIN: ACI  
; DEVELOPMENTAL STAGE: Adult  
; CELL TYPE: Splenocyte  
; FEATURE:  
; NAME/KEY: Rat scTLA-4

; IDENTIFICATION METHOD: Found by experiment  
; OTHER INFORMATION: B7 binding protein  
; US-08-804-180C-4

Query Match 14.6%; Score 92; DB 3; Length 174;  
Best Local Similarity 29.5%; Pred. No. 0.0085;  
Matches 36; Conservative 19; Mismatches 49; Indels 18; Gaps 7;

QY 3 VSQPEIRTLGSSAFIPC---SFNASQGRLAIGSVTWFRDEVPCKEVNGTPEFRGR 58  
Db 40 VTQPSVVLASSHGVSAPFCEYASSHNTDEVTVLRQT--NDQVT---EVCATFTVKNT 94

QY 59 LA----PLASSRFLHDHQAELHIRDVGRHDSIYVCVEVL---GLGVGTGNGTRL-VVE 110  
Db 95 LGFLDDPFCSGTTF-NESRVNLTIOQLRAADTGLYFCKVELMYPYPYFVGNGGTQIVIA 153

QY 111 KE 112

Db 154 KE 155

## RESULT 8

US-09-171-945-89  
; Sequence 89, Application US/09171945  
; Patent No. 6277599  
; GENERAL INFORMATION:

; APPLICANT: Emery, Stephen  
; APPLICANT: Copley, Clive Graham  
; APPLICANT: Edge, Michael Derek  
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
; TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System

```
; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-89

Query Match          14.2%; Score 89.5; DB 3; Length 120;
Best Local Similarity 27.8%; Pred. No. 0.01;
Matches 32; Conservative 10; Mismatches 34; Indels 39; Gaps 6;

QY 2 WVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG---TPERRG 57
Db 36 WVRQPP-----GR-GLGWIGWIDPE-----NGDTEYAPKFRG 66

QY 58 RLAPLASSRFLPHQAEHLHVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
Db 67 RATWLADS---SKNQASRLSSVTAADTAVYCHVLIYAGYLANDYWGQGTILTV 118

RESULT 9
US-08-804-180C-2
; Sequence 2, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: Mature Polypeptide
; ORIGINAL SOURCE:

; FILE REFERENCE: Monoclonal Antibody to CEA
; CURRENT APPLICATION NUMBER: US/09/171,945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
; US-09-171-945-89

Query Match          14.2%; Score 89.5; DB 3; Length 120;
Best Local Similarity 27.8%; Pred. No. 0.01;
Matches 32; Conservative 10; Mismatches 34; Indels 39; Gaps 6;

QY 2 WVSQPPPIRTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNG---TPERRG 57
Db 36 WVRQPP-----GR-GLGWIGWIDPE-----NGDTEYAPKFRG 66

QY 58 RLAPLASSRFLPHQAEHLHVRGHDASIYVCRVEVLGLGVGT---GNGTRLVV 109
Db 67 RATWLADS---SKNQASRLSSVTAADTAVYCHVLIYAGYLANDYWGQGTILTV 118

RESULT 9
US-08-804-180C-2
; Sequence 2, Application US/08804180C
; Patent No. 6107056
; GENERAL INFORMATION:
; APPLICANT: Martin K. Oaks
; TITLE OF INVENTION: sCTLA-4 and Its Soluble Products
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas M. Wozny
; STREET: 100 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 inch Disk
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,180C
; FILING DATE: February 20, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas M. Wozny
; REGISTRATION NUMBER: 28,922
; REFERENCE/DOCKET NUMBER: 3284-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 271-7590
; TELEFAX: (414) 271-5770
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: Mature Polypeptide
; ORIGINAL SOURCE:
```

```
; ORGANISM: Homo Sapien
; DEVELOPMENTAL STAGE: Adult
; TISSUE TYPE: Lymphnode
; FEATURE:
; NAME/KEY: Human sCTLA-4
; IDENTIFICATION METHOD: Found by experiment
; OTHER INFORMATION: Asn 76 and Asn 108 represent N-linked glycosylation; B7 binds
; US-08-804-180C-2

Query Match          14.2%; Score 89.5; DB 3; Length 137;
Best Local Similarity 25.2%; Pred. No. 0.012;
Matches 33; Conservative 18; Mismatches 59; Indels 21; Gaps 4;

QY 3 VSQPPEIRLTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEVRNGTPEFRGLIAPL 62
Db 3 VAQPAVVLASSRGIAISFVCEY-ASPGKATEVRVTILRQADSQVTEVCAATYMMGNELT-- 59
QY 63 ASSEFLHD-----HQAELHIVRGRHDASIYVCRVEVL-----GLGVGTGNGTRLV 108
Db 60 ----FLDDSICTGTSSGNQNLTIQGLRAMDTGLYICKVELMYPPPYLIGNGTQIYVI 115
QY 109 VEKEHPQLGAG 119
Db 116 AKEKKPSYNRG 126

RESULT 10
PCT-US95-15696-2
; Sequence 2, Application PC/TUS9515696
; GENERAL INFORMATION:
; APPLICANT: President and Fellows of Harvard College
; TITLE OF INVENTION: SINGLE CHAIN T-CELL RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,915
; FILING DATE: 06-DEC-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: HU-9404 WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-15696-2

Query Match          14.2%; Score 89.5; DB 5; Length 391;
Best Local Similarity 27.6%; Pred. No. 0.048;
Matches 34; Conservative 17; Mismatches 49; Indels 23; Gaps 7;

QY 6 PPEIRLTLEGSSAFPCSFNASQGRLAIGSVTWFRDEVVPGKEV-----RNGTPEFRGR 58
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Db 31 PQALISQEGENATNCSYKTS-----INLQWTRQN--SGRGLVHLILIRSRERKHSR 83  
QY 59 L-APLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGT-NGTRLVVEKEHPQL 116  
Db 84 LRVTLDTSK---KSSLLITATRAADTASYFCATDTGGSYIPTFGRTSLIV---HPSS 136  
QY 117 GAG 119  
Db 137 GGG 139

RESULT 11  
US-09-311-784A-32  
; Sequence 32, Application US/09311784A  
; Patent No. 6534482  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; PRIOR FILING DATE: 1999-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 32  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human MB-1 Ig-alpha  
US-09-311-784A-32

Query Match 13.9%; Score 88; DB 4; Length 226;  
Best Local Similarity 29.9%; Pred. No. 0.035;  
Matches 38; Conservative 13; Mismatches 50; Indels 26; Gaps 7;  
QY 1 LWSQ-PPEIRTLGSSAFIPCSFNASQGRLAIGSVTWFRDEVVPGKEVNGT--PEFRG 57  
Db 33 LWMKVPASLMVSLGEDAHPQCHNSSNN-----ANVTWR--VLHG---NYTWPEFLG 82  
QY 58 RLAPLASSRFLHDHQAELHIRDVRGHDASIYVCRVEVLGLGVGTNGTRLVVEKEHPQ-- 115  
Db 83 P-----GEDPNGTLTIONVKGHGIYVCRVQEGNESYQQSCGTYLVRVQPPRPF 133  
QY 116 --LGAGT 120  
Db 134 LDMGEGT 140

RESULT 12  
PCT-US95-08493-13  
; Sequence 13, Application PC/TUS9508493  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Clive  
; APPLICANT: Caruso, Anthony  
; TITLE OF INVENTION: Novel mlk Receptor Tyrosine Kinases  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LEGAL AFFAIRS  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02140

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/08493  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A  
; REGISTRATION NUMBER: 32,724  
; REFERENCE/DOCKET NUMBER: GI5234A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 498-8224  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 946 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-08493-13

Query Match 13.9%; Score 88; DB 5; Length 946;  
Best Local Similarity 29.3%; Pred. No. 0.23;  
Matches 27; Conservative 13; Mismatches 24; Indels 28; Gaps 5;  
QY 3 VSQPEIRTLGSSAFIPCSFNASQGRLAIG-----SVTWFRDEVVPGKEVNGTPEFRGR 58  
Db 126 IRPPTDVRALLGSKVLPCS-----TMGNPXPALISWFKDETA----LKNDQF----R 169  
QY 59 LAPLASSRFLHDHQAELHIRDVRGHDASIYVC 90  
Db 170 TSVLES-----GNLRNVQLEDAGKYRC 193

RESULT 13  
US-09-472-087-102  
; Sequence 102, Application US/09472087  
; Patent No. 6682736  
; GENERAL INFORMATION:  
; APPLICANT: HANSON, DOUGLAS C.  
; APPLICANT: NEVEU, MARK J.  
; APPLICANT: MUELLER, BILLEN E.  
; APPLICANT: HANKE, JEFFREY H.  
; APPLICANT: GILMAN, STEVEN C.  
; APPLICANT: DAVIS, C. GEOFFREY  
; APPLICANT: CORVALAN, JOSE R.  
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4  
; FILE REFERENCE: ABX-PFI  
; CURRENT APPLICATION NUMBER: US/09/472,087  
; CURRENT FILING DATE: 1999-12-23  
; PRIOR APPLICATION NUMBER: 60/113,647  
; PRIOR FILING DATE: 1998-12-23  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 102  
; LENGTH: 120  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-472-087-102

Query Match 13.8%; Score 87.5; DB 4; Length 120;  
Best Local Similarity 27.4%; Pred. No. 0.017;  
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;  
QY 3 VSQPEIRTLGSSAFIPCSFNASQGRLAIGSVTWFRDEVVPGKEVNGTPEFRGLAPL 62  
Db 3 VAQPAVILASSRGIASFVCEY-ASPGKATEVRVTLVROADSQVTEVCAATYMMGNELT-- 59  
QY 63 ASSRFLHD-----HQAELHIRDVRGHDASIYVCRVEVL---GLGVGTNGTRLVWE 110

Db 60 -----FLDDSICTSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGNGTQIYVI 115

Qy 111 KEHP 114

Db 116 DPEP 119

## RESULT 14

US-08-067-684-14  
; Sequence 14, Application US/08067684  
; Patent No. 5434131  
; GENERAL INFORMATION:  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Ledbetter, Jeffrey A.  
; APPLICANT: Damle, Nitin K.  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Suite 900  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 91101

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/067,684  
; FILING DATE: 26-MAY-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Adriano, Sarah B.  
; REGISTRATION NUMBER: 34,470  
; REFERENCE/DOCKET NUMBER: 7848-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 310/312-9900  
; TELEFAX: 310/479-8340  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-067-684-14

Query Match 13.8%; Score 87.5; DB 1; Length 187;  
Best Local Similarity 27.4%; Pred. No. 0.031;  
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

Qy 3 VSOPPEIRTELGSAFLPCSFNASQGLAIGSVTWPRDEWVPGKEVNRGTPEFRGLAPL 62

Db 4 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLQRADSQVTEVCAATYMGNELT-- 60

Qy 63 ASSRFLHD-----HQAEHLIRVGRHDSIYVCRVEVL---GLGVGTGNGTRLVVE 110

Db 61 -----FLDDSICTSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGNGTQIYVI 116

Qy 111 KEHP 114

Db 117 DPEP 120

## RESULT 15

US-08-008-898-14  
; Sequence 14, Application US/08008898  
; Patent No. 5770197  
; GENERAL INFORMATION:

; APPLICANT: Linsley, Peter S  
; APPLICANT: Ledbetter, Jeffrey A  
; APPLICANT: Damle, Nitin K  
; APPLICANT: Brady, William  
; TITLE OF INVENTION: CTLA4 RECEPTOR AND METHODS FOR ITS USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheldon & Mak  
; STREET: 201 South Lake Avenue, Suite 800  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: United States  
; ZIP: 91101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,898  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/723,617  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandel, Saralynn  
; REGISTRATION NUMBER: 31,853  
; REFERENCE/DOCKET NUMBER: 7848  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 187 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-008-898-14

Query Match 13.8%; Score 87.5; DB 1; Length 187;  
Best Local Similarity 27.4%; Pred. No. 0.031;  
Matches 34; Conservative 15; Mismatches 56; Indels 19; Gaps 4;

Qy 3 VSOPPEIRTELGSAFLPCSFNASQGLAIGSVTWPRDEWVPGKEVNRGTPEFRGLAPL 62

Db 4 VAQPAVVLASSRGIAFVCEY-ASPGKATEVRVTVLQRADSQVTEVCAATYMGNELT-- 60

Qy 63 ASSRFLHD-----HQAEHLIRVGRHDSIYVCRVEVL---GLGVGTGNGTRLVVE 110

Db 61 -----FLDDSICTSGNQVNLTIQGLRAMDTGLYICKVELMYPYPYLGNGTQIYVI 116

Qy 111 KEHP 114

Db 117 DPEP 120

Search completed: November 16, 2004, 19:17:43

Job time : 34.7401 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 3.93103 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-5  
Perfect score: 88  
Sequence: 1 VLLLRAGFYAVSFLSVAVG 19  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	53.4	835	2	T06590
2	46	52.3	724	2	T04340
3	46	52.3	757	2	T03561
4	44.5	50.6	479	2	T34293
5	44	50.0	184	2	C90157
6	43	48.9	466	2	AH1800
7	43	48.9	581	2	S03540
8	42	47.7	217	2	F69512
9	42	47.7	271	2	B83918
10	42	47.7	388	2	B83228
11	42	47.7	466	2	A14426
12	42	47.7	560	2	S46096
13	42	47.7	658	2	S74246
14	41	46.6	310	2	F74027
15	41	46.6	333	2	A70602
16	41	46.6	356	2	A70332
17	41	46.6	364	2	H83787
18	41	46.6	451	2	E90171
19	41	46.6	498	2	T19901
20	40	45.5	135	2	E83466
21	40	45.5	154	2	F69477
22	40	45.5	233	2	C95987
23	40	45.5	245	2	I51323
24	40	45.5	288	2	T37709
25	40	45.5	303	2	T42703
26	40	45.5	328	2	C87673
27	40	45.5	342	2	AG3092
28	40	45.5	351	2	E64524
29	40	45.5	351	2	G71983

30 40 45.5 382 2 H86930 probable secreted  
31 40 45.5 401 2 F75037 hexuronate transpo  
32 40 45.5 412 2 F97196 probable permease,  
33 40 45.5 423 2 G71650 proline/betaine tr  
34 40 45.5 424 2 H97870 proline/betaine tr  
35 40 45.5 452 2 T45448 probable serine pr  
36 40 45.5 507 2 E90540 hypohethetical prote  
37 40 45.5 514 2 S46733 hypohethetical prote  
38 40 45.5 572 2 T13740 probable hormone r  
39 40 45.5 606 2 AC2425 Atp-binding protei  
40 40 45.5 610 2 A85870 probable transport  
41 40 45.5 610 2 H91025 probable transport  
42 40 45.5 610 2 B85001 probable transport  
43 40 45.5 1040 2 D81379 transmembrane effl  
44 39.5 44.9 396 2 AD3012 conserved hypoteth  
45 39.5 44.9 492 2 C98272 hypohethetical prote

#### ALIGNMENTS

##### RESULT 1

T06590  
probable beta-galactosidase (EC 3.2.1.23) - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06590  
R:Carey, A.T.; Holt, K.; Picard, S.; Wilde, R.; Tucker, G.A.; Bird, C.R.; Schuch, W.; S  
Plant Physiol. 108, 1099-1107, 1995  
A:Title: Tomato exo-(1-4)-beta-D-galactanase: isolation, changes during ripening in nor  
A:Reference number: 215780; MUID:95357407; PMID:7630937  
A:Accession: T06590  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-835 <CAR>  
A:Cross-references: UNIPROT:P48980; EMBL:X83854; NID:G971484; PIDN:CAA58734.1; PID:G971  
A:Experimental source: Cultivar Ailsa Craig; pericarp  
C:Superfamily: beta-galactosidase bga  
C:Keywords: glycosidase; hydrolase

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 8.6;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
||| :|||

Db 527 LRAGNKISLLSIAVG 542  
||| :|||

##### RESULT 2

T04340  
beta-galactosidase (EC 3.2.1.23) II precursor - tomato  
C:Species: Lycopersicon esculentum (tomato)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04340  
R:Smith, D.L.; Starrett, D.A.; Gross, K.C.  
Plant Physiol. 117, 417-423, 1998  
A:Title: A gene coding for tomato fruit beta-galactosidase II is expressed during fruit  
A:Reference number: 215296; MUID:98289087; PMID:9625694  
A:Accession: T04340  
A>Status: translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-724 <SMI>  
A:Cross-references: UNIPROT:O81100; EMBL:AF020390; NID:G3299895; PIDN:AAC25984.1; PID:G  
A:Experimental source: strain Rutgers; tissue-type tomato fruit  
C:Genetics:  
A:Gene: Bgal4  
C:Superfamily: beta-galactosidase bga  
C:Keywords: glycosidase; hydrolase  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-724/Product: beta-galactosidase II #status predicted <MAT>

Query Match 52.3%; Score 46; DB 2; Length 724;

```

Best Local Similarity 62.5%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLSVAVG 19
||||| : |||||
529 LRAGINKISLLSVSVG 544

DB

RESULT 3
T02561
probable cellulose synthase At2g32620 [imported] - Arabidopsis thaliana
N;Alternate names: cellulose synthase homolog T26B15.18
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02561; D84735
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence.
A;Reference number: Z14678
A;Accession: T02561
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-757 <ROU>
A;Cross-references: UNIPROT:O80899; EMBL:AC004681; NID:g3298532; PID:g3298550
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VarAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MID:20083487; PMID:10617197
A;Accession: D84735
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-757 <STO>
A;Cross-references: GB:AE002093; NID:g3298550; PIDN:AAC25944.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g32620; T26B15.18
A;Map position: 2
A;Introns: 88/2; 194/3; 236/3; 277/3; 344/3; 390/1; 450/3; 566/3

Query Match 52.3%; Score 46; DB 2; Length 757;
Best Local Similarity 58.8%; Pred. No. 11;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 LRAGFYAVSFSLSVAVG 19
||||| : |||||
740 LRAGFLAVSFVFSVG 756

DB

RESULT 4
T31293
aldehyde dehydrogenase homolog - Sphingomonas aromaticivorans plasmid pNL1
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T31293
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati
A;Reference number: Z20992
A;Accession: T31293
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-479 <ROM>
A;Cross-references: UNIPROT:O86001; EMBL:AF079317; NID:g3378261; PID:g3378434; PIDN:AA0
C;Genetics:
A;Genome: plasmid pNL1
A;Note: nahP
C;Superfamily: NAD-dependent aldehyde dehydrogenase; aldehyde dehydrogenase homology

Query Match 50.6%; Score 44.5; DB 2; Length 479;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 3; Indels 3; Gaps 1;

```

QY     3 LLRAGF---YAVSFSLVAVG 19  
       :|||||:|||||  
DB     95 IAKAGFETRFVAVSFLRAAIG 114

RESULT 5

C90157  
hypothetical protein SSO0169 [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: C90157  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: C90157  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-184 <KUR>  
A;Cross-references: UNIPROT:Q98OV8; GB:AE006641; MID:g138l13300; PIDN:AAK40514.1; CSPDB:S  
C;Genetics:  
A;Gene: SSO0169

Query Match           50.0%; Score 44; DB 2; Length 184;  
Best Local Similarity 75.0%; Pred. No. 6.3;  
Matches      9; Conservative   1; Mismatches   2; Indels   0; Gaps   0;

QY     3 LLRAGFYAVSFL 14  
       :|||||||  
DB     76 LISAGLYAVSFL 87

RESULT 6

AH1800  
transmembrane efflux protein homolog lin2951 [imported] - Listeria innocua (strain Clip1)  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AH1800  
R;Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunat, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
C.; Title: Comparative genomics of *Listeria species.*  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AH1800  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-466 <GLA>  
A;Cross-references: UNIPROT:Q926T9; GB:AL592022; PIDN:CAC98176.1; PID:g16415492; CSPDB:G  
A;Experimental source: strain Clip1262  
C;Genetics:  
A;Gene: lin2951  
C;Superfamily: multidrug-efflux transporter

Query Match           48.9%; Score 43; DB 2; Length 466;  
Best Local Similarity 58.8%; Pred. No. 23;  
Matches     10; Conservative   1; Mismatches   6; Indels   0; Gaps   0;

QY     2 LLRAGFYAVGSFLSVAV 18  
       ||| ||| |  
DB     434 LITNVGFVVLSISAV 450

RESULT 7

S03540  
gene frizzled protein precursor - fruit fly (*Drosophila melanogaster*)  
C;Species: *Drosophila melanogaster*  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004

C/Accession: S03540; S15708; S15709  
R/Vinson, C.R.; Conover, S.; Adler, P.N.  
Nature 338, 263-264, 1989  
A/Title: A *Drosophila* tissue polarity locus encodes a protein containing seven potential  
A/Reference number: S03540; MUID:89159415; PMID:2493583  
A/Accession: S03540  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-581 <VIN>  
A/Cross-references: UNIPROT:P18537  
R/Adler, P.N.; Vinson, C.; Park, W.J.; Conover, S.; Klein, L.  
Genetics 126, 401-416, 1990  
A/Title: Molecular structure of a frizzled, a *Drosophila* tissue polarity gene.  
A/Reference number: S15708; MUID:91060073; PMID:2174014  
A/Accession: S15708  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-581 <ADL>  
A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38460.1; PID:g804979  
A/Accession: S15709  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-405, 'WV', 408, 'WOFHTIN' <AD2>  
A/Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38461.1; PID:g804980  
C/Genetics:  
A/Gene: FlyBase: fz  
A/Cross-references: FlyBase:FBgn0001085  
A/Intons: 224/3; 264/3; 329/3; 405/1  
C/Superfamily: fruit fly frizzled protein  
C/Keywords: alternative splicing; transmembrane protein  
F/1-26/Donain: signal sequence #status predicted <SIG>  
F/27-591/Product: gene frizzled protein #status predicted <MAT>  
  
Query Match 48.9%; Score 43; DB 2; Length 581;  
Best Local Similarity 50.0%; Pred. No. 28;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
  
QY 2 LLIRAGFYAVSFLSVAVG 19  
DB 468 LMLRIGFFSGLFILPAVG 485  
  
RESULT 8  
F69512  
conserved hypothetical protein AF2102 - *Archaeoglobus fulgidus*  
C/Species: *Archaeoglobus fulgidus*  
C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C/Accession: F69512  
R/Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A/Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A/Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A/Reference number: A69250; MUID:98049343; PMID:9389475  
A/Accession: F69512  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-217 <KLE>  
A/Cross-references: UNIPROT:O28178; GB:AE000958; GB:AE000782; NID:g2689281; PIDN:AAB8914  
  
Query Match 47.7%; Score 42; DB 2; Length 217;  
Best Local Similarity 76.9%; Pred. No. 16;  
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 LLIRAGFYAVSFL 14  
DB 198 LLLSAGLAVSFL 210  
  
RESULT 9  
B86918

hypothetical protein glpQ [imported] - *Mycobacterium leprae*  
C/Species: *Mycobacterium leprae*  
C/Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C/Accession: B86918  
R/Cole, S.T.; Eigemeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H  
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S  
A/Title: Massive gene decay in the leprosy bacillus.  
A/Reference number: A86909; MUID:21128732; PMID:111234002  
A/Accession: B86918  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-271 <STO>  
A/Cross-references: UNIPROT:Q9CDC5; GB:AL450380; NID:gl3092456; PIDN:CAC29582.1; GSPDB:  
C/Genetics:  
A/Gene: glpQ  
  
Query Match 47.7%; Score 42; DB 2; Length 271;  
Best Local Similarity 57.9%; Pred. No. 20;  
Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 VLLIRAGFYAVSFLSVAVG 19  
DB 184 VLLGRAGRYLTSSAATAVG 202  
  
RESULT 10  
B83228  
Probable MFS transporter PA3336 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C/Species: *Pseudomonas aeruginosa*  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C/Accession: B83228  
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laczbig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path  
A/Reference number: A82950; MUID:20437337; PMID:10984043  
A/Accession: B83228  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-388 <STO>  
A/Cross-references: UNIPROT:Q9HYQ9; GB:AE004756; GB:AE004966; PIDN:AAG067.  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: PA3336  
C/Superfamily: Streptomyces lividans chloramphenicol resistance protein  
  
Query Match 47.7%; Score 42; DB 2; Length 388;  
Best Local Similarity 53.3%; Pred. No. 28;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 5 RAGFYAVSFLSVAVG 19  
DB 157 RASFFAVALVAVLVG 171  
  
RESULT 11  
A11426  
transmembrane efflux protein homolog lmo2818 [imported] - *Listeria monocytogenes* (strain  
C/Species: *Listeria monocytogenes*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C/Accession: A11426  
R/Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; M  
ck, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
A/Title: Comparative Genomics of *Listeria* species.  
A/Reference number: AB1077; MUID:21537279; PMID:11679669

A/Accession: A11426  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-466 <GLA>  
 A/Cross-references: UNIPROT:Q8V3L7; GB:NC\_003210; PID:G16412318; GSPDB:  
 A/Experimental source: strain EGD-e  
 C/Genetics:  
 A/Gene: lmc2818  
 C/Superfamily: multidrug-efflux transporter

Query Match 47.7%; Score 42; DB 2; Length 466;  
 Best Local Similarity 52.9%; Pred. No. 33;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVSFSLVAV 18  
 |||||  
 Db 434 LLTNVGFVVLSLISVAI 450

RESULT 12  
 S46096  
 probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae)  
 N/Alternate names: hypothetical protein YBR1510  
 C/Species: Saccharomyces cerevisiae  
 C/Date: 26-Aug-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: S46096  
 R/Dubois, E.; El Bakoury, M.; Glansdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;  
 submitted to the Protein Sequence Database, August 1994  
 A/Reference number: S45782  
 A/Accession: S46096  
 A/Molecule type: DNA  
 A/Residues: 1-560 <DUE>  
 A/Cross-references: UNIPROT:P38318; EMBL:Z36088; NID:G536611; GSPDB:GN00002  
 A/Experimental source: strain S288C  
 C/Genetics:  
 A/Gene: MIPS:YBR220C  
 A/Cross-references: SGD:S0000424  
 A/Map position: 2R  
 C/Keywords: transmembrane protein  
 F/18-37/Domain: transmembrane #status predicted <TM01>  
 F/88-106/Domain: transmembrane #status predicted <TM02>  
 F/139-155/Domain: transmembrane #status predicted <TM03>  
 F/177-193/Domain: transmembrane #status predicted <TM04>  
 F/218-238/Domain: transmembrane #status predicted <TM05>  
 F/330-347/Domain: transmembrane #status predicted <TM06>  
 F/391-407/Domain: transmembrane #status predicted <TM07>  
 F/421-437/Domain: transmembrane #status predicted <TM08>  
 F/475-491/Domain: transmembrane #status predicted <TM09>  
 F/521-544/Domain: transmembrane #status predicted <TM10>

Query Match 47.7%; Score 42; DB 2; Length 560;  
 Best Local Similarity 36.8%; Pred. No. 40;  
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 VLLRAGFYAVSFSLVAV 19  
 |||||  
 Db 516 VTILRDGYITNLICIVWG 534

RESULT 13  
 S74246  
 sulfate transport protein - Arabidopsis thaliana  
 N/Alternate names: sulfate transporter  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 28-Oct-1996 #sequence\_revision 14-Nov-1997 #text\_change 09-Jul-2004  
 C/Accession: S74246  
 R/Takahashi, H.; Sasaki, N.; Noji, M.; Saito, K.  
 FEBS Lett. 392, 95-99, 1996  
 A/Title: Isolation and characterization of a cDNA encoding a sulfate transporter from A.  
 A/Reference number: S74246; MUID:96368029; PMID:8772182  
 A/Accession: S74246  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA

A/Residues: 1-658 <TAK>  
 A/Cross-references: UNIPROT:P92946; EMBL:D85416; NID:G1498119; PID:G1498120  
 C/Superfamily: sulfate transport protein  
 C/Keywords: sulfate transport; transmembrane protein  
 F/92-109/Domain: transmembrane #status predicted <TM1>  
 F/119-134/Domain: transmembrane #status predicted <TM2>  
 F/140-156/Domain: transmembrane #status predicted <TM3>  
 F/172-190/Domain: transmembrane #status predicted <TM4>  
 F/194-217/Domain: transmembrane #status predicted <TM5>  
 F/253-271/Domain: transmembrane #status predicted <TM6>  
 F/278-299/Domain: transmembrane #status predicted <TM7>  
 F/338-353/Domain: transmembrane #status predicted <TM8>  
 F/371-388/Domain: transmembrane #status predicted <TM9>  
 F/408-430/Domain: transmembrane #status predicted <TM10>  
 F/435-457/Domain: transmembrane #status predicted <TM11>  
 F/464-489/Domain: transmembrane #status predicted <TM12>

Query Match 47.7%; Score 42; DB 2; Length 658;  
 Best Local Similarity 50.0%; Pred. No. 46;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LLLRAGFYAVSFSLVAVG 19  
 |||||  
 Db 465 LVLIAPFGVLFASVEIG 482

RESULT 14  
 F71027  
 hypothetical protein PHI514 - Pyrococcus horikoshii  
 C/Species: Pyrococcus horikoshii  
 C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
 C/Accession: F71027  
 R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatai, Y.; Yamamoto, S.; Seki,  
 M.; Ohkubo, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a  
 A/Reference number: A71000; MUID:98344137; PMID:9679194  
 A/Accession: F71027  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-310 <KAW>  
 A/Cross-references: UNIPROT:O59183; GB:AP000006; NID:G3236133; PIDN:BAA30622.1; PID:G325  
 A/Experimental source: strain OT3  
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C/Genetics:  
 A/Gene: PHI514

Query Match 46.6%; Score 41; DB 2; Length 310;  
 Best Local Similarity 59.3%; Pred. No. 33;  
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 FYAVSFSLVAVG 19  
 |||||  
 Db 34 YYLAFSLGVG 45

RESULT 15  
 A70602  
 hypothetical protein Rv0998 - Mycobacterium tuberculosis (strain H37RV)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
 C/Accession: A70602  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 ; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; MUID:98295987; PMID:9634230  
 A/Accession: A70602  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-333 <COL>

A;Cross-references: UNIPROT:O05581; GB:Z94752; GB:AL123456; NID:G3261731; PIDN:CAB08156.  
A;Experimental source: strain H37Rv  
C;Genetics:  
A;Gene: RV0998

Query Match 46.6%; Score 41; DB 2; Length 333;  
Best Local Similarity 55.6%; Pred. No. 35;  
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 2 LLRAGFYAVSFLSVAVG 19  
:|||||:|:|:  
Db 46 VLLRQGEPAVSFLLISSG 63

Search completed: November 16, 2004, 19:15:54  
Job time : 6.93103 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 16, 2004, 18:56:15 ; Search time 21.2175 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-5  
Perfect score: 88  
Sequence: 1 VLLLRAGFYAVSLVAVG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	176	1 NCT3_MACFA	P61483 macaca fasc
2	88	100.0	201	1 NCT3_HUMAN	O14931 homo sapien
3	88	100.0	201	1 NCT3_PANTR	P61484 pan troglod
4	85	96.6	180	1 NCT3_MACMU	O8m102 macaca mula
5	70	79.5	192	1 NCT3_RAT	O8cfd9 rattus norv
6	51	58.0	847	2 O9SCW1	O9scw1 arabidopsis
7	51	58.0	847	2 O8RNC1	O8rnc1 arabidopsis
8	49	55.7	610	2 Q7VEF7	Q7vef7 prochloroco
9	48	54.5	707	2 O6S761	O6s761 cicor ariet
10	48	54.5	721	2 Q9ZP30	Q9z30 carica papa
11	47	53.4	571	2 O6BUP5	O6bup5 debaryomyce
12	47	53.4	835	1 EGAL_LYCES	P48980 lycopersico
13	47	53.4	835	2 CAA10174	Caa10174 lycopersi
14	47	53.4	835	2 AAF21626	Aaf21626 lycopersi
15	47	53.4	838	2 Q9ZP11	Q9z11 lycopersico
16	46	52.3	724	2 O81100	O81100 lycopersico
17	46	52.3	724	2 Q9TOP6	Q9top6 lycopersico
18	46	52.3	757	2 O80899	O80899 arabidopsis
19	46	52.3	3763	2 O8T2A1	O8t2a1 dictyosteli
20	45	51.1	230	2 Q7X9C6	Q7x9c6 pyrus pyrif
21	45	51.1	270	2 Q8RD77	Q8rd77 thermoanaer
22	45	51.1	376	2 Q3FVH5	Q3fvh5 prunus arme
23	45	51.1	843	2 Q93X58	Q93x58 fragaria an
24	45	51.1	1561	2 Q888F2	O888f2 pseudomonas
25	44.5	50.6	479	2 O86001	O86001 sphingomona
26	44	50.0	146	2 Q70121	Q70121 oncorhynch
27	44	50.0	146	2 CAE45583	Cae45583 oncorhync
28	44	50.0	184	2 Q880V8	Q880v8 sulfolobus
29	44	50.0	351	2 Q8G3L8	Q8g3l8 bifidobacte
30	44	50.0	381	1 Q46A_DROME	Q46a drosophila
31	44	50.0	476	2 Q82WR1	Q82wr1 nitrosomona

32	44	50.0	591	2 Q79YS2	Q79ys2 streptococc
33	44	50.0	591	2 Q8K8X7	Q8k8x7 streptococc
34	44	50.0	591	2 Q8P300	Q8p300 streptococc
35	44	50.0	602	2 Q8CR29	Q8cr29 staphylococ
36	44	50.0	739	2 Q9M5J3	Q9m5j3 phaseolus a
37	44	50.0	826	2 Q6EM02	Q6em02 sandersonia
38	44	50.0	845	2 Q9LLS9	Q9lls9 lycopersico
39	43.5	49.4	202	2 Q8BW87	Q8bw87 mus musculu
40	43.5	49.4	306	2 Q8BX24	Q8bx24 mus musculu
41	43.5	49.4	334	2 Q8BKX2	Q8bkx2 mus musculu
42	43.5	49.4	355	1 S3SD_HUMAN	Q9ritn3 homo sapien
43	43	48.9	85	2 Q6BI02	Q6bi02 debaryomyce
44	43	48.9	160	2 Q8M0F0	Q8m0f0 cryptococcu
45	43	48.9	202	2 Q85T00	Q85t00 cryptococcu

ALIGNMENTS

RESULT 1  
NCT3\_MACFA  
ID NCT3\_MACFA STANDARD; PRT; 176 AA.  
AC P61483; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
DE Name=NCR3;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopithecinae; Macaca.  
OC NCBI\_TaxID=9541;  
RN [1]\_TaxID=9541;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoid;  
RA Rizzi M., Biassoni R.;  
RT "Non MHC specific natural cytotoxicity receptors (NCR) expressed in Macaca fascicularis lymphoid cells."  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
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CC -----  
CC EMBL; AJ279389; CAC41081.1; -;  
CC HSP; P16410; 1185.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; IG\_1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS50835; IG\_LIKE; 1.  
CC Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane. Potential.  
FT SIGNAL 1 18  
FT CHAIN 19 176  
FT Natural cytotoxicity triggering receptor 3.  
FT DOMAIN 19 135  
FT Extracellular (Potential).  
FT TRANSMEM 136 156  
FT Potential.  
FT DOMAIN 157 176  
FT Cytoplasmic (Potential).  
FT DOMAIN 19 126  
FT IG-like.  
FT DISULFID 39 108  
FT By similarity.

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;

Query Match 100.0%; Score 88; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 2,7e+06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19  
 DB 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 2

NCT3\_HUMAN STANDARD; PRT; 201 AA.  
 ID NCT3\_HUMAN O14930; O14932; O95667; O95668; O95669;  
 AC O14931; O14932; O14933; O14934; O14935;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
 DE cell p30-related protein) (Nkp30) (NK-P30).  
 GN Name=NCR3; Synonyms=IC7;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBT\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH  
 RP CD3Z, AND FUNCTION.  
 RC TISSUE=Lymphoid;  
 RA PubMed=10562324;  
 RX Fende D., Parolini S., Pessino A., Sivori S., Augugliaro R.,  
 RA Morelli L., Marsenaro E., Accame L., Malaspina A., Biassoni R.,  
 RA Bottino C., Moretta L., Moretta A.;  
 RT "Identification and molecular characterization of Nkp30, a novel  
 RT triggering receptor involved in natural cytotoxicity mediated by human  
 RT natural killer cells.";  
 RL J. Exp. Med. 190:1505-1516(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
 RP WITH CD3Z.  
 RC TISSUE=Peripheral blood;  
 RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K.,  
 RA Fuji T.;  
 RT "Identification of two novel single nucleotide polymorphisms in the  
 RT Nkp30 gene in human natural killer cells.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
 RX MEDLINE=99218514; PubMed=10202016;  
 RA Neville M.J., Campbell R.D.;  
 RT "A new member of the Ig superfamily and a V-ATPase G subunit are among  
 RT the predicted products of novel genes close to the TNF locus in the  
 RT human MHC.";  
 RL J. Immunol. 162:4745-4754(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=Spleen;  
 RX MEDLINE=9642187; PubMed=8824804;  
 RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
 RT "Genes in a 220-kb region spanning the TNF cluster in human MHC.";  
 RL Genomics 31:215-222(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX PubMed=1465967; DOI=10.1101/gr.1736803;  
 RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,  
 RA Campbell R.D., Hood L.;  
 RT "Analysis of the gene-dense major histocompatibility complex class III  
 RT region and its comparison to mouse.";  
 RL Genome Res. 13:2621-2636(2003).  
 RN [6]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).

RA Shiina S., Tamiya G., Oka A., Inoko H.;  
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Blood;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
 CC the increased efficiency of activated natural killer (NK) cells to  
 CC mediate tumor cell lysis.  
 CC -!- SUBUNIT: Interacts with CD3Z.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=6;  
 CC Name=1; Synonyms=IC7a;  
 CC IsoId=O14931-1; Sequence=Displayed;  
 CC Note=No experimental confirmation available;  
 CC Name=2; Synonyms=IC7c;  
 CC IsoId=O14931-2; Sequence=VSP\_010413;  
 CC Note=No experimental confirmation available;  
 CC Name=3; Synonyms=IC7b;  
 CC IsoId=O14931-3; Sequence=VSP\_010412;  
 CC Note=No experimental confirmation available;  
 CC Name=4; Synonyms=IC7e;  
 CC IsoId=O14931-4; Sequence=VSP\_010411;  
 CC Note=No experimental confirmation available;  
 CC Name=5; Synonyms=IC7f;  
 CC IsoId=O14931-5; Sequence=VSP\_010411, VSP\_010413;  
 CC Note=No experimental confirmation available;  
 CC Name=6; Synonyms=IC7d;  
 CC IsoId=O14931-6; Sequence=VSP\_010411, VSP\_010412;  
 CC Note=No experimental confirmation available;  
 CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
 CC activated NK cells and weakly expressed in spleen.  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
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 CC -----  
 CC EMBL; AJ223153; CAB54004.1; -;  
 CC EMBL; AB055881; BAB78472.1; -;  
 CC EMBL; Y14768; CAA75063.1; -;  
 CC EMBL; Y14768; CAA75064.1; -;  
 CC EMBL; Y14768; CAA75065.1; -;  
 CC EMBL; Y14768; CAA75066.1; -;  
 CC EMBL; Y14768; CAA75067.1; -;  
 CC EMBL; Y14768; CAA75068.1; -;







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Genome Res. 14:631-639(2004).
-!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).
-!- SUBUNIT: Interacts with CD3Z (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC -----
DR EMBL; AJ430418; CAD23066.1; -
DR EMBL; AJ430419; CAD23067.2; -
DR EMBL; AJ430420; CAD23067.2; JOINED.
DR EMBL; AY273824; AAP13457.1; -
DR EMBL; BX383046; CAE84000.1; -
DR HSP; P09793; IDQT.
DR RGD; 727881; 1C7.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 192 Natural cytotoxicity triggering receptor
FT FT 3.
FT FT DOMAIN 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT DOMAIN 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 IG-like.
FT DISULFID 39 108 By similarity.
FT VARIANT 7 7 I -> V.
FT VARIANT 19 19 I -> V.
FT VARIANT 82 82 A -> T.
FT VARIANT 138 138 A -> V.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB25D22377 CRC64;

Query Match 79.5%; Score 70; DB 1; Length 192;
Best Local Similarity 83.3%; Pred. No. 0.0027;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLRLAGFYAVSFLSVAVG 19
||||| |||||
DB 148 LLRLAGVYALSFLSVATG 165

RESULT 6
Q9SCW1 PRELIMINARY; PRT; 847 AA.
ID Q9SCW1 AC Q9SCW1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23).
GN Name=SGAU1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP Gy I., Kreis M., Lecharny A.;
RA Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AY093197; AAM13196.1; --  
 DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
 DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000922; Gal\_lectin.  
 DR InterPro; IPR001944; Glyco\_hydro\_35.  
 DR InterPro; IPR002016; Peroxidase.  
 DR Pfam; PF02140; Gal\_lectin; 1.  
 DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
 DR PRINTS; PR00742; GLHYDRLASE35.  
 DR PRODOM; PD005612; Gal\_lectin; 1.  
 DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
 DR PROSITE; PS00435; PEROXIDASE\_1; UNKNOWN\_1.  
 DR PROSITE; PS50228; SUEL\_LECTIN; 1.  
 KW Glycosidase; Hydrolase.  
 SQ SEQUENCE 847 AA; 93672 MW; 0F9E12685426C5DA CRC64;  
 Query Match 58.0%; Score 51; DB 2; Length 847;  
 Best Local Similarity 62.5%; Pred. No. 13;  
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 LRAGFYAVSFSLVAVG 19  
 Db 539 LRAGFNKIALSLVAVG 554  
 RESULT 8  
 Q7VEF7  
 ID Q7VEF7 PRELIMINARY; PRT; 610 AA.  
 AC Q7VEF7;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE ABC-type multidrug transport system ATPase and permease components.  
 GN Name=mdlb; OrderedLocusNames=Pro00056;  
 OS Prochlorococcus marinus.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;  
 OC Prochlorococcus.  
 CX NCBI\_TaxID=1219;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SARG / CCMP 1375 / SS120;  
 RX MEDLINE=22810154; PubMed=12917486;  
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., Wolf Y.I., Hess W.R.;  
 RA "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).  
 CC -!- SIMILARITY: Belongs to the ABC transporter family.  
 DR EMBL; AE017161; AAP99102.1; --  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR011527; ABC\_membrane\_1.  
 DR InterPro; IPR001140; ABC\_TM\_transp.  
 DR InterPro; IPR003439; ABC\_transporter.  
 DR Pfam; PF00664; ABC\_membrane; 1.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR PRODOM; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS50929; ABC\_TM1F; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.  
 DR PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.

KW ATP-binding; Complete proteome.  
 SQ SEQUENCE 610 AA; 68701 MW; EBF39690CS16DCDA CRC64;  
 Query Match 55.7%; Score 49; DB 2; Length 610;  
 Best Local Similarity 44.4%; Pred. No. 21;  
 Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 VLLLRAGFYAVSFSLVAV 18  
 Db 156 ILQIVSGFFIVSFISAI 173  
 RESULT 9  
 O65761  
 ID O65761 PRELIMINARY; PRT; 707 AA.  
 AC O65761;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-galactosidase (EC 3.2.1.23) (Fragment).  
 OS Cicer arietinum (Chickpea) (Garbanzo).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.  
 CX NCBI\_TaxID=3827;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Etisolated epicotyl;  
 RA Dopico B., Batehan R., Labrador E.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.  
 CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.  
 DR EMBL; AJ006771; CA07236.1; --  
 DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
 DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
 DR GO; GO:0005529; F:sugar binding; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR000922; Gal\_lectin.  
 DR InterPro; IPR001944; Glyco\_hydro\_35.  
 DR Pfam; PF02140; Gal\_lectin; 1.  
 DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
 DR PRINTS; PR00742; GLHYDRLASE35.  
 DR PRODOM; PD005612; Gal\_lectin; 1.  
 DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
 DR PROSITE; PS50228; SUEL\_LECTIN; 1.  
 KW Glycosidase; Hydrolase.  
 FT NON TER 1  
 SQ SEQUENCE 707 AA; 77903 MW; 85C970DDA8A92A31 CRC64;  
 Query Match 54.5%; Score 48; DB 2; Length 707;  
 Best Local Similarity 68.8%; Pred. No. 35;  
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 LRAGFYAVSFSLVAVG 19  
 Db 399 LRAGWNKISLSVAVG 414  
 RESULT 10  
 Q9ZP30  
 ID Q9ZP30 PRELIMINARY; PRT; 721 AA.  
 AC Q9ZP30;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Beta-galactosidase precursor (EC 3.2.1.23).  
 OS Carica papaya (Papaya).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eucosids II; Brassicales; Caricaceae; Carica.

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OX NCBI_TaxID=3649;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mesocarp;
RA Othman R., Chco T.S., Ali Z.M., Zainal Z., Lazan H.;
RT "A full-length beta-galactosidase cDNA sequence from ripening
RL papaya.";
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
DR EMBL; AF647486; AAC7377.1; -.
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008979; Gal bind like.
DR InterPro; IPR001944; Glyco_hydro_35.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 721 beta galactosidase.
SQ SEQUENCE 721 AA; 80985 MW; 841BF5E16C399617 CRC64;

Query Match 54.5%; Score 48; DB 2; Length 721;
Best Local Similarity 68.8%; Pred. No. 36;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19
Db 526 LRAGVNKSLLSIAVG 541
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RESULT 11
O6BUP5 PRELIMINARY; PRT; 571 AA.
AC Q8BUP5
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P38318 Saccharomyces cerevisiae YBR220c.
GN ORFNames=DEHAC0100439;
OC Debaryomyces hansenii (Yeast) (Torulasporea hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=4959;
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Tallia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennecuin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Ozias S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Svennene D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RA Genoscode;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; CR382135; CAG86145.1; -.
SQ SEQUENCE 571 AA; 63970 MW; 02E730425004ABBD CRC64;

Query Match 53.4%; Score 47; DB 2; Length 571;
Best Local Similarity 47.4%; Pred. No. 43;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
Db 525 VLLLRAGFYAVSFSLVAVG 19
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RESULT 12
BGAL LYCES
ID BGAL LYCES STANDARD; PRT; 835 AA.
AC P48980;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Beta-galactosidase precursor (EC 3.2.1.23) (Lactase) (Acid beta-
DE galactosidase) (Exo-(1-->4)-beta-D-galactanase).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC STRAIN=cv. Ailsa Craig; TISSUE=Pericarp;
RX MEDLINE=96357407; PubMed=7630937;
RA Carey A.T., Holt K., Picard S., Wilde R., Tucker G.A., Bird C.R.,
RA Schuch W., Seymour G.B.;
RT "Tomato exo-(1-->4)-beta-D-galactanase. Isolation, changes during
RT ripening in normal and mutant tomato fruit, and characterization of a
RT related cDNA clone.";
RL Plant Physiol. 108:1099-1107 (1995).
CC -!- FUNCTION: Involved in cell wall degradation. Degrades
CC polysaccharides containing beta-(1-->4)-linked galactans, acting
CC as an exo-(1-->4)-beta-D-galactanase.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-
CC galactose residues in beta-D-galactosides.
CC -!- MISCELLANEOUS: Has a pH optimum of 4.5.
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.
CC -!- SIMILARITY: Contains 1 SUEL-type lectin domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83854; CAA58734.1; -.
DR PIR; T06590; T06590.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR000922; Gal_lectin.
DR InterPro; IPR001944; Glyco_hydro_35.
DR Pfam; PF01301; Gal_lectin; 1.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
DR PRODOM; PD005612; Gal_lectin; 1.
DR PROSITE; PS01182; GLYCOSYL_HYDROL_F35; 1.
DR PROSITE; PS0228; SUEL_LECTIN; 1_22.
KW Direct protein sequencing; Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 22
FT CHAIN 23 835 Beta-galactosidase.
FT DOMAIN 749 835 SUEL-type lectin.
FT ACT_SITE 180 180 Proton donor (Potential).
FT ACT_SITE 249 249 Nucleophile (Potential).
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95CA646 CRC64;

Query Match 53.4%; Score 47; DB 1; Length 835;

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Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVNIKISLSIAVG 542

RESULT 13  
CAA10174 PRELIMINARY; PRT; 835 AA.

AC CAA10174;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE SS-galactosidase precursor (EC 3.2.1.23).  
GN TEG1B.

OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
OC Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Money maker;  
RA De Silva J.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ012797; CAA10174.1; -  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 835 SS-GALACTOSIDASE.  
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95C4A646 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVNIKISLSIAVG 542

RESULT 14  
AAF21626 PRELIMINARY; PRT; 835 AA.

AC AAF21626;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Beta-galactosidase precursor.  
GN TBG1.

OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;  
OC Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Rutgers; TISSUE=fruit;  
RX MEDLINE=98289087; PubMed=9625694;  
RA Smith D.L., Starratt D.A., Gross K.C.;  
RT "A gene coding for tomato fruit beta-galactosidase II is expressed during fruit ripening. Cloning, characterization, and expression pattern."  
RT Plant Physiol. 117:417-423(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. Rutgers; TISSUE=fruit;  
RA Smith D.L., Gross K.C.;  
RT "A family of at least seven beta-galactosidase genes is expressed during tomato fruit development."  
RL Plant Physiol. 123:1173-1183(2000).  
DR EMBL; AF023847; AAF21626.1; -  
KW Signal.

FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 835 BETA-GALACTOSIDASE.  
SQ SEQUENCE 835 AA; 93336 MW; 94C9685F95C4A646 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 835;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 527 LRAGVNIKISLSIAVG 542

RESULT 15  
Q9ZP11 PRELIMINARY; PRT; 838 AA.

AC Q9ZP11;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE SS-galactosidase precursor (EC 3.2.1.23).  
GN Name=teglA;  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA De Silva J., Jarman C., Strongitharm B., Gidley M.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-galactose residues in beta-D-galactosides.  
CC -!- SIMILARITY: Belongs to family 35 of glycosyl hydrolases.  
DR EMBL; AJ012796; CAA10173.1; -  
DR GO; GO:0009341; C:beta-galactosidase complex; IEA.  
DR GO; GO:0004565; F:beta-galactosidase activity; IEA.  
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.  
DR GO; GO:0005529; F:sugar binding; IEA.  
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro; IPR008979; Gal\_bind like.  
DR InterPro; IPR008922; Gal\_lectin.  
DR InterPro; IPR001944; Glyco\_hydro\_35.  
DR Pfam; PF01301; Glyco\_hydro\_35; 1.  
DR PRINTS; PR00742; GLHYDRLASE35.  
DR PRODOM; PD005612; Gal\_lectin; 1.  
DR PROSITE; PS01182; GLYCOSYL\_HYDROL\_F35; 1.  
DR PROSITE; PS0228; SUEL\_LECTIN; 1.  
KW Glycosidase; Hydrolase; Signal.  
FT SIGNAL 1 25  
FT CHAIN 26 838 ss-galactosidase.  
SQ SEQUENCE 838 AA; 92923 MW; AC2E11ABFA417762 CRC64;

Query Match 53.4%; Score 47; DB 2; Length 838;  
Best Local Similarity 62.5%; Pred. No. 60;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
DB 530 LRAGVNIKISLSIAVG 545

Search completed: November 16, 2004, 19:14:33  
Job time : 24.4175 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 20.2095 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFSLVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	19	4	Aae02772 Human Nkp
2	88	100.0	19	8	Adq30925 Human Nkp
3	88	100.0	177	2	Aay06402 Human B-C
4	88	100.0	190	2	Aay06401 Human B-C
5	88	100.0	190	4	Aae02769 Human Nkp
6	88	100.0	190	8	Ado19810 Human PRO
7	88	100.0	190	8	Adq30923 Human Nkp
8	88	100.0	201	2	Aay06403 Human B-C
9	80	90.9	19	5	Aae23900 Human Nkp
10	51	58.0	274	3	Aag23590 Arabidops
11	51	58.0	279	3	Aag23589 Arabidops
12	48	54.5	665	6	Aao16046 Carica pa
13	48	54.5	665	6	Aae32202 Papaya be
14	48	54.5	721	6	Aao16048 Carica pa
15	48	54.5	721	6	Aae32204 Papaya be
16	47	53.4	835	3	Aay44303 Tomato be
17	47	53.4	838	2	Aar2882 Tomato ex
18	47	53.4	838	3	Aay44305 Tomato be
19	46	52.3	114	3	Aag05624 Arabidops
20	46	52.3	119	3	Aag05623 Arabidops
21	46	52.3	127	3	Aag05622 Arabidops
22	46	52.3	651	3	Aag42606 Arabidops
23	46	52.3	714	3	Aag42605 Arabidops
24	46	52.3	724	3	Aay44306 Tomato be
25	46	52.3	757	3	Aag42604 Arabidops

26	46	52.3	757	5	AB991980	Ab91980 Herbicida
27	45	51.1	1563	6	ABU41824	Abu41824 Protein e
28	44	50.0	87	7	ADC97632	Adc97632 E. faeciu
29	44	50.0	385	3	AA320910	Aab20910 Drosophil
30	44	50.0	385	7	AD215306	Add15306 Fruitfly
31	44	50.0	417	4	AA811928	Aag81928 S. epider
32	44	50.0	425	5	ABP66312	Abp66312 Bifidobac
33	44	50.0	602	5	ABP39571	Abp39571 Staphyloc
34	44	50.0	602	6	ABU42891	Abu42891 Protein e
35	43.5	49.4	355	7	ADJ69975	Adj69975 Human hea
36	43.5	49.4	383	6	ABO00770	Ab000770 Polypepti
37	43	48.9	154	6	ABO00816	Ab000816 Polypepti
38	43	48.9	166	6	AB866413	Ab866413 Drosophil
39	43	48.9	469	4	AA376682	Aab76682 Corynebac
40	43	48.9	530	4	AA376681	Aab76681 Corynebac
41	43	48.9	530	4	AA379761	Aab79761 Corynebac
42	43	48.9	536	7	ADG74257	Adg74257 Fruit fly
43	43	48.9	578	4	AA90808	Aag90808 C glutami
44	43	48.9	589	4	AB571245	Ab571245 Drosophil
45	42	47.7	271	6	ABU35719	Abu35719 Protein e

#### ALIGNMENTS

RESULT 1  
AAE02772  
ID AAE02772 standard; peptide; 19 AA.  
XX  
AC AAE02772;  
XX  
AC AAE02772;  
DT 06-AUG-2001 (first entry)  
XX  
DE Human Nkp30 receptor transmembrane region sequence.  
XX

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
XX melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
XX immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
XX therapy; transmembrane region.  
XX

OS Homo sapiens.

XX WO200136630-A2.  
XX  
XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.  
XX  
PR 15-NOV-1999; 99CA-02288307.  
PR 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.  
XX (UYGE-) UNIV GENOVA.  
XX  
PI Moretta A, Bottino C, Biassoni R;  
XX  
XX WPI; 2001-329221/34.

XX Novel compound, useful for detection and/or quantifying the presence of  
XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.  
XX  
XX Claim 1; Fig 7B; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA  
XX molecule which is involved in natural cytotoxicity mediated by natural  
XX killer (NK) cells and antibodies that identify the same Nkp30 receptor  
XX is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively  
XX expressed on the surface of human mature NK cells. Nkp30 and its cDNA are  
XX useful for detecting and/or quantifying the presence of NK cells in a  
XX biological sample. The invention also provide kits for detecting and/or  
XX quantifying the presence of NK cells, for the selective removal of NK  
XX cells from a biological sample, for the positive and selective  
XX purification of NK cells from a biological sample and for the in vitro

CC stimulation of NK cell cytotoxicity. The invention further provides a  
CC pharmaceutical composition which is used as a drug for grafting  
CC enhancement, graft versus host (GVH) inhibition, stimulation of graft  
CC versus tumour (GVT) and especially graft versus leukaemia (GVL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. Nkp30 antibodies are useful for  
CC identifying Nkp30 natural ligands and allow assessment of the level of  
CC surface Nkp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence Nkp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is the transmembrane region of human Nkp30 receptor  
XX  
XX  
SQ Sequence 19 AA;

Query Match 100.0%; Score 88; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
DB 1 VLLLRAGFYAVSFLSVAVG 19

RESULT 2  
ADQ30925  
ID ADQ30925 standard; protein; 19 AA.  
AC ADQ30925;  
XX  
XX 23-SEP-2004 (first entry)  
XX Human Nkp30 transmembrane region.  
XX Natural killer cell; NK cell; Nkp30; cytostatic; antimicrobial.

XX Homo sapiens.  
XX WO2004056392-A1.  
XX 08-JUL-2004.  
XX 22-DEC-2003; 2003WO-EP014716.  
XX 23-DEC-2002; 2002US-0435344P.  
XX (INNA-) INNATE PHARMA.  
XX Romagne F, Andre P;  
XX WPI; 2004-507595/48.  
XX  
XX Pharmaceutical compositions that stimulate proliferation of natural  
XX killer cells useful for therapy of melanoma, chronic myeloid, and  
XX leukemia, comprise an anti-natural killer cell receptor antibody and  
XX interleukins.  
XX Claim 3; SEQ ID NO 3; 35pp; English.

XX The present sequence is that of the transmembrane region of human Nkp30  
XX ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
XX natural killer (NK) cells, and particularly by mature NK cells. Claimed  
XX pharmaceutical compositions that have a stimulating effect on the  
XX proliferation of NK cells comprise an antibody such as an anti-Nkp30  
XX antibody or anti-Nkp46 antibody or its immuno-reactive fragment and a  
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
XX antibody(ies) and cytokine(s) being administered together or separately  
XX to a subject. The anti-Nkp30 antibody is an isolated antibody or its  
XX antigen-binding fragment which specifically binds to Nkp30 or to a  
XX fragment, including the transmembrane region, of Nkp30. The  
XX pharmaceutical compositions, when used for daily subcutaneous injection,  
XX comprising from 1 ng to 100 mg/kg (body weight) of antibody(ies), and  
XX lower than 1 million units/square meters/day of cytokine(s), are useful

CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,  
CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
CC prevention, palliation and therapy (claimed).

XX Sequence 19 AA;  
Query Match 100.0%; Score 88; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VLLLRAGFYAVSFLSVAVG 19  
DB 1 VLLLRAGFYAVSFLSVAVG 19

RESULT 3  
AAY06402  
ID AAY06402 standard; protein; 177 AA.  
XX  
XX AAY06402;  
XX  
XX 20-SEP-1999 (first entry)  
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX  
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
XX signal transduction; immunomodulator; antiinflammatory;  
XX autoimmune disease; inflammation; gene therapy; diagnosis.  
XX Homo sapiens.

XX Key Location/Qualifiers  
XX Peptide 1..12 /note= "leader peptide"  
XX Protein 13..177 /note= "mature protein"  
XX Modified-site 42 /note= "N-glycosylated"  
XX Modified-site 58 /note= "N-glycosylated"  
XX Modified-site 121 /note= "N-glycosylated"  
XX Domain 139..162 /note= "transmembrane domain"  
XX Peptide 166..177 /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.  
XX  
XX 20-MAY-1999.  
XX  
XX 05-NOV-1998; 98WO-US023826.  
XX  
XX 07-NOV-1997; 97US-0064761P.  
XX  
XX (BIOJ) BIOGEN INC.  
XX  
XX Browning J;  
XX  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59348.  
XX  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX  
XX Claim 2; Page 43; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
XX oligodendrocyte glycoprotein family that is expressed by germinal centre  
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
XX identified. The protein is present primarily in the spleen, in lymph  
XX nodes and in germinal centre B cells. It may have immunoregulatory  
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to



CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 177 AA;

Query Match 100.0%; Score 88; DB 2; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
 Db 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 4

AA06401  
 ID AAY06401 standard; protein; 190 AA.

XX AC AAY06401;

XX DT 20-SEP-1999 (first entry)

XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.

XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.

XX OS Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..12 /note= "leader peptide"
FT Protein	13..190 /note= "mature protein"
FT Modified-site	42 /note= "N-glycosylated"
FT Modified-site	68 /note= "N-glycosylated"
FT Modified-site	121 /note= "N-glycosylated"
FT Domain	139..162 /note= "transmembrane domain"
FT Peptide	165..190 /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.

XX 20-MAY-1999.

XX 05-NOV-1998; 98WO-US023826.

XX 07-NOV-1997; 97US-0064761P.

XX (BIOJ ) BIOGEN INC.

XX Browning J;

XX WPI; 1999-418423/35.

XX N-PSDB; AAX59347.

XX Novel B-cell myelin oligodendrocyte glycoproteins.

XX Claim 2; Page 42; 43pp; English.

XX This sequence represents human BMOG, a novel member of the B cell myelin  
 CC oligodendrocyte glycoprotein family that is expressed by germinal centre

CC B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
 CC identified. The protein is present primarily in the spleen, in lymph  
 CC nodes and in germinal centre B cells. It may have immunoregulatory  
 CC functions, and soluble or chimeric fusion proteins of BMOG may be used to  
 CC regulate the immune system in autoimmune or inflammatory disease. Vectors  
 CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
 CC producing BMOG using these transformed host cells are also provided. BMOG  
 CC polypeptides can be used for modulating the immune system of a subject or  
 CC to inhibit signal transduction in a cell expressing BMOG by contacting it  
 CC with a soluble BMOG protein. The nucleic acid can be used for gene  
 CC therapy. The protein can also be used to target a toxin, imaging agent or  
 CC radionuclide to a cell expressing BMOG. (All claimed)

XX Sequence 190 AA;

Query Match 100.0%; Score 88; DB 2; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-07;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
 Db 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 5

AAE02769  
 ID AAE02769 standard; protein; 190 AA.

XX AC AAE02769;

XX DT 06-AUG-2001 (first entry)

XX DE Human Nkp30 receptor.

XX KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
 KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
 KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
 KW therapy.

XX OS Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..18 /label= "Signal_peptide"
FT Protein	19..190 /label= "Mature_Nkp30_receptor_protein"
FT Region	19..138 /label= "Extracellular_region"
FT Modified-site	42 /note= "N-glycosylation site"
FT Modified-site	121 /note= "N-glycosylation site"
FT Region	139..157 /label= "Transmembrane_region"
FT Region	158..190 /label= "Intracellular_region"

XX WO200136630-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

DR N-PSDB; AAD06564.

XX Novel compound, useful for detection and/or quantifying the presence of

XX NK cells, comprises the amino acid sequences of the NKp30 molecule.

XX

XX Claim 1; Fig 7B; 83pp; English.

XX

XX The invention relates to human NKp30 receptor and its corresponding cDNA

XX molecule which is involved in natural cytotoxicity mediated by natural

XX killer (NK) cells and antibodies that identify the same. NKp30 receptor

XX is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively

XX expressed on the surface of human mature NK cells. NKp30 and its cDNA are

XX useful for detecting and/or quantifying the presence of NK cells in a

XX biological sample. The invention also provide kits for detecting and/or

XX quantifying the presence of NK cells, for the selective removal of NK

XX cells from a biological sample, for the positive and selective

XX purification of NK cells from a biological sample and for the in vitro

XX stimulation of NK cell cytotoxicity. The invention further provides a

XX pharmaceutical composition which is used as a drug for grafting

XX enhancement, graft versus host (GVH) inhibition, stimulation of graft

XX versus tumour (GVT) and especially graft versus leukaemia (GvL), and for

XX the prevention, palliation and/or therapy of solid or liquid tumours,

XX such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or

XX microorganism, notably viral infection. NKp30 antibodies are useful for

XX identifying NKp30 natural ligands and allow assessment of the level of

XX surface NKp30 ligand expressed on an NK-susceptible target cell and the

XX comparison of this level to the standard physiological one. Hence NKp30

XX antibodies are useful in the diagnosis of tumours or of infection. The

XX present sequence is human NKp30 receptor

XX

XX Sequence 190 AA;

XX

XX Query Match 100.0%; Score 88; DB 4; Length 190;

XX Best Local Similarity 100.0%; Pred. No. 8.4e-07;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 VILLRAGFYAVSFSLVAVG 19

DB 139 VILLRAGFYAVSFSLVAVG 157

RESULT 6

ADO19810

ID ADO19810 standard; protein; 190 AA.

XX

XX ADO19810;

XX

DT 12-AUG-2004 (first entry)

XX

XX Human PRO polypeptide #367.

XX

XX Human; PRO; immune related disorder; systemic lupus erythematosus;

XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;

XX systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;

XX autoimmune hemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;

XX diabetes mellitus; renal disease; demyelinating disease;

XX central nervous system; peripheral nervous system;

XX demyelinating polyneuropathy; Guillain-Barre syndrome;

XX chronic inflammatory demyelinating polyneuropathy.

XX

XX Homo sapiens.

XX

XX WO2004043361-A2.

XX

PN 27-MAY-2004.

XX

XX

XX 06-NOV-2003; 2003WO-US035268.

XX

XX

XX 08-NOV-2002; 2002US-0425235P.

XX

XX (GETH ) GENENTECH INC.

XX

XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;

XX

```

PA (INNA-) INNATE PHARMA.
XX
XX Romagne F, Andre P;
XX WPI; 2004-507595/48.
XX
XX Pharmaceutical compositions that stimulate proliferation of natural
XX killer cells useful for therapy of melanoma, chronic myeloid, and
XX leukemia, comprise an anti-natural killer cell receptor antibody and
XX interleukins.
XX
XX Claim 3; SEQ ID NO 1; 35pp; English.
XX
XX The present sequence is that of human NKp30, a 190 amino acid polypeptide
XX (about 30 kDa on SDS-PAGE) that is selectively expressed by natural
XX killer (NK) cells, and particularly by mature NK cells. Claimed
XX pharmaceutical compositions that have a stimulating effect on the
XX proliferation of NK cells comprise an antibody such as an anti-NKp30
XX antibody or anti-NKp46 antibody or its immuno-reactive fragment and a
XX cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the
XX antibody(ies) and cytokine(s) being administered together or separately
XX to a subject. The anti-NKp30 antibody is an isolated antibody or its
XX antigen-binding fragment which specifically binds to NKp30 or to a
XX fragment ADQ10924-ADQ10927 of NKp30. The pharmaceutical compositions,
XX when used for daily subcutaneous injection, comprising from 1 ng to 100
XX mg/kg (body weight) of antibody(ies), and lower than 1 million
XX units/square meters/day of cytokine(s), are useful for the prevention,
XX palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute
XX myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung
XX adenocarcinoma, neuroblastoma and for antimicrobial prevention,
XX palliation and therapy (claimed).
XX
XX Sequence 190 AA;
XX
XX Query Match 100.0%; Score 88; DB 8; Length 190;
XX Best Local Similarity 100.0%; Pred. No. 8.4e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19
Db 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 8
AA06403
ID AA06403 standard; protein; 201 AA.
AC AA06403;
XX
XX 20-SEP-1999 (first entry)
XX
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.
XX
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;
XX signal transduction; immunomodulator; antiinflammatory;
XX autoimmune disease; inflammation; gene therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..12
XX /note= "leader peptide"
XX Protein 13..201
XX /note= "mature protein"
XX Modified-site 42
XX /note= "N-glycosylated"
XX Modified-site 68
XX /note= "N-glycosylated"
XX Modified-site 121
XX /note= "N-glycosylated"
XX Domain 139..162
XX /note= "transmembrane domain"
XX Peptide 166..201

/alternatively spliced C-terminal end"
WO9923867-A2.
20-MAY-1999.
05-NOV-1998; 98WO-US023826.
07-NOV-1997; 97US-0064761P.
(BIOC ) BIOGEN INC.
Browning J;
WPI; 1999-418423/35.
N-PSDB; AAX59349.
Novel B-cell myelin oligodendrocyte glycoproteins.
Claim 2; Page 43; 43pp; English.
This sequence represents human BMOG, a novel member of the B cell myelin
oligodendrocyte glycoprotein family that is expressed by germinal centre
B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were
identified. The protein is present primarily in the spleen, in lymph
nodes and in germinal centre B cells. It may have immunoregulatory
functions, and soluble or chimeric fusion proteins of BMOG may be used to
regulate the immune system in autoimmune or inflammatory disease. Vectors
comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
producing BMOG using these transformed host cells are also provided. BMOG
polypeptides can be used for modulating the immune system of a subject or
to inhibit signal transduction in a cell expressing BMOG by contacting it
with a soluble BMOG protein. The nucleic acid can be used for gene
therapy. The protein can also be used to target a toxin, imaging agent or
radionuclide to a cell expressing BMOG. (All claimed)
XX
XX Sequence 201 AA;
XX
XX Query Match 100.0%; Score 88; DB 2; Length 201;
XX Best Local Similarity 100.0%; Pred. No. 8.9e-07;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19
Db 139 VLLLRAGFYAVSFLSVAVG 157

RESULT 9
AAE23900
ID AAE23900 standard; peptide; 19 AA.
AC AAE23900;
XX
XX 10-SEP-2002 (first entry)
XX
XX Human NKp30 receptor peptide.
XX
XX KAR-associated protein; KARAP-transduced immune signal; dendritic cell;
XX antigen presentation; contact sensitivity; multiple sclerosis;
XX neuroprotective; human; NKp30 receptor peptide.
XX
XX Homo sapiens.
XX
XX WO200224940-A2.
XX
XX 28-MAR-2002.
XX
XX 20-SEP-2001; 2001WO-EP011492.
XX
XX 20-SEP-2000; 2000US-0234161P.
XX
XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX

```

PI Vivier E, Vely F, Tomasello E;  
 XX WPI; 2002-454420/48.  
 XX  
 PT Identifying KAR-associated protein-transduced immune signal inhibitor,  
 PT comprises using cells co-expressing functional KARAP, and engineered  
 PT cells and animals that over-express functional KARAP or bear non-  
 PT functional KARAP.  
 XX  
 XX Example 4; Page 45; 89pp; English.  
 PS  
 CC The present invention relates to a novel method for identifying compounds  
 CC capable of inhibiting KAR-associated protein (KARAP)-transduced immune  
 CC signals. The method involves using functional and non-functional KARAP,  
 CC cells co-expressing functional KARAP, functional receptors transducing  
 CC their signal by zeta, gamma or epsilon and engineered cells and animals  
 CC over-expressing functional KARAP or bearing non-functional KARAP. The  
 CC method is useful for identifying compounds capable of inhibiting KARAP-  
 CC transduced immune signals. The KARAP-inhibiting compounds are useful for  
 CC impairing the development and maturation of dendritic cells, for  
 CC inhibiting the antigen presentation of dendritic cells, for synthesis  
 CC inhibition or through inhibition of the migration of dendritic cells, for  
 CC making drugs intended for inhibiting dendritic cell development or  
 CC maturation, for preparing drugs for the treatment, prevention, palliation  
 CC of immune response, where the activation of KAR has to be inhibited and  
 CC for the treatment of contact sensitivity or multiple sclerosis. The  
 CC present sequence is human NKp30 receptor peptide which associate with CD3  
 CC zeta and FcR gamma. This sequence is used in the exemplification of the  
 CC invention  
 XX  
 SQ Sequence 19 AA;  
 Query Match 90.9%; Score 80; DB 5; Length 19;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LLRAGFYAVSFLSVAVG 19  
 Db 1 LLRAGFYAVSFLSVAVG 17  
 RESULT 10  
 AAG23590  
 ID AAG23590 standard; protein; 274 AA.  
 XX  
 AC AAG23590;  
 XX  
 DT 17-OCT-2000 (first entry)  
 XX  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 26954.  
 XX  
 DE Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PP 25-FEB-2000; 2000EP-00301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 03-MAR-1999; 99US-01233548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 23-MAR-1999; 99US-0126264P.  
 PR 23-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128234P.  
 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
 PR 19-APR-1999; 99US-0130077P.  
 PR 21-APR-1999; 99US-0130449P.  
 PR 23-APR-1999; 99US-0130510P.  
 PR 23-APR-1999; 99US-0130891P.  
 PR 28-APR-1999; 99US-0131449P.  
 PR 30-APR-1999; 99US-0132048P.  
 PR 30-APR-1999; 99US-0132407P.  
 PR 04-MAY-1999; 99US-0132484P.  
 PR 05-MAY-1999; 99US-0132485P.  
 PR 06-MAY-1999; 99US-0132486P.  
 PR 06-MAY-1999; 99US-0132487P.  
 PR 07-MAY-1999; 99US-0132863P.  
 PR 11-MAY-1999; 99US-0134256P.  
 PR 14-MAY-1999; 99US-0134218P.  
 PR 14-MAY-1999; 99US-0134219P.  
 PR 14-MAY-1999; 99US-0134221P.  
 PR 14-MAY-1999; 99US-0134370P.  
 PR 18-MAY-1999; 99US-0134768P.  
 PR 19-MAY-1999; 99US-0134941P.  
 PR 20-MAY-1999; 99US-0135124P.  
 PR 21-MAY-1999; 99US-0135333P.  
 PR 24-MAY-1999; 99US-0135629P.  
 PR 25-MAY-1999; 99US-0136021P.  
 PR 27-MAY-1999; 99US-0136392P.  
 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138094P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
 PR 16-JUN-1999; 99US-0139453P.  
 PR 17-JUN-1999; 99US-0139492P.  
 PR 18-JUN-1999; 99US-0139454P.  
 PR 18-JUN-1999; 99US-0139455P.  
 PR 18-JUN-1999; 99US-0139456P.  
 PR 18-JUN-1999; 99US-0139457P.  
 PR 18-JUN-1999; 99US-0139458P.  
 PR 18-JUN-1999; 99US-0139459P.  
 PR 18-JUN-1999; 99US-0139460P.  
 PR 18-JUN-1999; 99US-0139461P.  
 PR 18-JUN-1999; 99US-0139462P.  
 PR 18-JUN-1999; 99US-0139463P.  
 PR 18-JUN-1999; 99US-0139750P.  
 PR 18-JUN-1999; 99US-0139763P.  
 PR 21-JUN-1999; 99US-0139817P.  
 PR 22-JUN-1999; 99US-0139899P.  
 PR 23-JUN-1999; 99US-0140353P.  
 PR 23-JUN-1999; 99US-0140354P.  
 PR 24-JUN-1999; 99US-0140635P.  
 PR 28-JUN-1999; 99US-0140823P.  
 PR 29-JUN-1999; 99US-0140991P.  
 PR 30-JUN-1999; 99US-0141287P.  
 PR 01-JUL-1999; 99US-0141842P.  
 PR 01-JUL-1999; 99US-0142154P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 06-JUL-1999; 99US-0142330P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
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Query Match 58.0%; Score 51; DB 3; Length 274;
Best Local Similarity 62.5%; Fred. No. 2.7;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LRAGFYAVSF*SVAVG 19
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Db 30 LRAGFNKIALLSIAGV 45

RESULT 11
AAG23589
ID AAG23589 standard; protein; 279 AA.
XX
AC AAG23589;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26953.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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 DB 35 LRAGFNKIALISIAVG 50

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 ID AAO16046 standard; protein; 665 AA.  
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 AC AAO16046;  
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 DT 27-FEB-2003 (first entry)  
 XX  
 DE Carica papaya beta-galactosidase (Beta-gal-45).  
 XX  
 KW Enzyme; papaya; beta-galactosidase; pectinmethylesterase;  
 KW polygalacturonase; fruit ripening.  
 XX  
 OS Carica papaya.  
 XX  
 FN WO200283924-A2.  
 XX  
 FD 24-OCT-2002.  
 XX  
 EF 11-APR-2002; 2002WO-US011804.  
 XX  
 PR 11-APR-2001; 2001US-0283008P.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 PA (PAIS/) PAIS M S S.  
 XX  
 PI Pais MSS, Gonsalves D, Balde A;  
 XX  
 DR WPI; 2003-075556/07.  
 DR N-PSDB; AAL51072.  
 XX  
 PT New isolated nucleic acid molecule encoding beta-galactosidase protein,  
 PT useful for promoting or delaying papaya fruit ripening.  
 XX  
 PS Claim 3; Page 9-13; 84pp; English.  
 XX  
 CC The invention comprises the amino acid and coding sequence of Carica  
 CC papaya beta-galactosidase proteins which control papaya fruit ripening.  
 CC The invention also comprises the amino acid and coding sequence of Carica  
 CC papaya pectinmethylesterase and polygalacturonase proteins. The DNA and  
 CC protein sequences of the invention are useful for promoting or delaying  
 CC papaya fruit ripening. The present amino acid sequence represents a  
 CC Carica papaya fruit ripening-related protein of the invention  
 XX  
 SQ Sequence 665 AA;

Query Match 54.5%; Score 48; DB 6; Length 665;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19  
 ||||| : : : : :  
 DB 383 LRAGINKISILSIIVG 398

RESULT 13  
 AAE32202  
 ID AAE32202 standard; protein; 665 AA.  
 XX  
 AC AAE32202;  
 XX  
 DT 24-MAR-2003 (first entry)  
 XX  
 DE Papaya beta-galactosidase (beta-Gal).45.  
 XX  
 KW Fruit ripening; papaya ringspot virus coat protein; transgenic plant;  
 KW transgenic; PRSV; CP; beta-galactosidase; beta-Gal.45; enzyme.  
 XX  
 OS Carica papaya.  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 143  
 FT /label= Unknown  
 FT /note= "Encoded by TGN"  
 XX  
 PN WO200282889-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 11-APR-2002; 2002WO-US011803.  
 XX  
 PR 11-APR-2001; 2001US-0283022P.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 PA (PAIS/) PAIS M S S.  
 XX  
 PI Pais MSS, Gonsalves D, Balde A, Chiang C;  
 XX  
 DR WPI; 2003-075493/07.  
 DR N-PSDB; AAD49832.  
 XX  
 PT New DNA construct, useful for controlling the ripening of papaya fruit  
 PT and conferring resistance to papaya ringspot virus coat in transgenic  
 PT plants.  
 XX  
 PS Disclosure; Page 75-77; 121pp; English.  
 XX  
 CC The invention relates to a DNA construct comprising a first DNA molecule  
 CC encoding a protein that controls papaya fruit ripening and a second DNA  
 CC molecule encoding a papaya ringspot virus (PRSV) coat protein (CP). The  
 CC DNA construct is useful for controlling the ripening of papaya fruit and  
 CC conferring resistance to PRSV coat in transgenic plants. The present  
 CC sequence is papaya beta-galactosidase (beta-Gal).45  
 XX  
 SQ Sequence 665 AA;

Query Match 54.5%; Score 48; DB 6; Length 665;  
 Best Local Similarity 62.5%; Pred. No. 24;  
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFSLVAVG 19  
 ||||| : : : : :  
 DB 383 LRAGINKISILSIIVG 398

RESULT 14  
 AAO16048  
 ID AAO16048 standard; protein; 721 AA.  
 XX

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AC AAO16048;
XX
XX 27-FEB-2003 (first entry)
XX
XX Carica papaya beta-galactosidase (Beta-gal-41).
XX
XX Enzyme; papaya; beta-galactosidase; pectinmethylesterase;
XX polygalacturonase; fruit ripening.
XX
XX Carica papaya.
XX
XX WO200283924-A2.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US011804.
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XX 11-APR-2001; 2001US-0283008P.
XX
XX (CORR ) CORNELL RES FOUND INC.
XX (PAIS//) PAIS M S S.
XX
XX Pais MSS, Gonsalves D, Balde A;
XX
XX WPI; 2003-075556/07.
XX N-PSDB; AALS1074.
XX
XX New isolated nucleic acid molecule encoding beta-galactosidase protein,
XX useful for promoting or delaying papaya fruit ripening.
XX
XX Claim 17; Page 15-19; 84pp; English.
XX
XX The invention comprises the amino acid and coding sequence of Carica
XX papaya beta-galactosidase proteins which control papaya fruit ripening.
XX The invention also comprises the amino acid and coding sequence of Carica
XX papaya pectinmethylesterase and polygalacturonase proteins. The DNA and
XX protein sequences of the invention are useful for promoting or delaying
XX papaya fruit ripening. The present amino acid sequence represents a
XX Carica papaya fruit ripening-related protein of the invention
XX
XX SQ Sequence 721 AA;
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XX Query Match 54.5%; Score 48; DB 6; Length 721;
XX Best Local Similarity 68.8%; Pred. No. 26;
XX Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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XX QY 4 LRAGFYAVSFLSVAVG 19
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XX RESULT 15
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XX ID AE32204 standard; protein; 721 AA.
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XX AC AE32204;
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XX 24-MAR-2003 (first entry)
XX
XX Papaya beta-galactosidase (beta-Gal).41.
XX
XX Fruit ripening; papaya ringspot virus coat protein; transgenic plant;
XX transgenic; PRSV; CP; beta-galactosidase; beta-Gal.41; enzyme.
XX
XX Carica papaya.
XX
XX WO200282889-A1.
XX
XX 24-OCT-2002.
XX
XX 11-APR-2002; 2002WO-US011803.
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XX 11-APR-2001; 2001US-0283022P.
XX

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XX (CORR ) CORNELL RES FOUND INC.
XX (PAIS//) PAIS M S S.
XX
XX Pais MSS, Gonsalves D, Balde A, Chiang C;
XX
XX WPI; 2003-075493/07.
XX N-PSDB; AAD49834.
XX
XX New DNA construct, useful for controlling the ripening of papaya fruit
XX and conferring resistance to papaya ringspot virus coat in transgenic
XX plants.
XX
XX Disclosure; Page 80-83; 121pp; English.
XX
XX The invention relates to a DNA construct comprising a first DNA molecule
XX encoding a protein that controls papaya fruit ripening and a second DNA
XX molecule encoding a papaya ringspot virus (PRSV) coat protein (CP). The
XX DNA construct is useful for controlling the ripening of papaya fruit and
XX conferring resistance to PRSV coat in transgenic plants. The present
XX sequence is papaya beta-galactosidase (beta-Gal).41
XX
XX SQ Sequence 721 AA;
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XX Query Match 54.5%; Score 48; DB 6; Length 721;
XX Best Local Similarity 68.8%; Pred. No. 26;
XX Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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XX QY 4 LRAGFYAVSFLSVAVG 19
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XX Search completed: November 16, 2004, 18:55:58
XX Job time : 24.2095 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 : Search time 16.9841 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:  
2: /cgn2\_6/ptodata/1/pubpaa/PCR\_NEW\_PUB.pep:  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:  
6: /cgn2\_6/ptodata/1/pubpaa/PCRUS\_PUBCOMB.pep:  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88	100.0	19	13	US-10-036-444-5
2	88	100.0	161	16	US-10-696-259-10
3	88	100.0	175	16	US-10-696-259-8
4	88	100.0	177	16	US-10-696-259-5
5	88	100.0	185	16	US-10-696-259-7
6	88	100.0	190	13	US-10-036-444-2
7	88	100.0	190	16	US-10-696-259-4
8	88	100.0	198	16	US-10-696-259-9
9	88	100.0	201	16	US-10-696-259-6
10	49	55.7	100	16	US-10-437-963-161934
11	48	54.5	428	15	US-10-424-599-207360
12	48	54.5	665	14	US-10-121-393-2
13	48	54.5	665	14	US-10-121-539-2

14	48	54.5	721	14	US-10-121-393-6
15	48	54.5	721	14	US-10-121-539-6
16	45	51.1	231	17	US-10-425-115-349552
17	45	51.1	250	15	US-10-425-114-48020
18	45	51.1	1563	15	US-10-282-122A-69748
19	44.5	50.6	473	14	US-10-369-493-10510
20	44	50.0	222	15	US-10-425-114-55971
21	44	50.0	247	15	US-10-425-114-40659
22	44	50.0	312	15	US-10-425-114-49039
23	44	50.0	385	15	US-10-601-309-20
24	44	50.0	392	15	US-10-425-114-43621
25	44	50.0	433	15	US-10-425-114-36786
26	44	50.0	493	15	US-10-424-599-246507
27	44	50.0	523	15	US-10-424-599-236336
28	44	50.0	602	15	US-10-282-122A-70815
29	44	50.0	727	15	US-10-425-114-52764
30	44	50.0	727	15	US-10-425-114-55408
31	44	50.0	739	15	US-10-424-599-262939
32	43.5	49.4	355	16	US-10-408-765A-1781
33	43	48.9	154	14	US-10-243-552-940
34	43	48.9	361	17	US-10-739-930-10917
35	43	48.9	469	15	US-10-627-476-346
36	43	48.9	530	15	US-10-627-476-344
37	43	48.9	536	10	US-09-847-102A-42
38	43	48.9	578	9	US-09-738-626-4562
39	42	47.7	65	15	US-10-424-599-242117
40	42	47.7	87	15	US-10-437-963-154905
41	42	47.7	271	15	US-10-282-122A-63643
42	42	47.7	388	15	US-10-389-647-564
43	42	47.7	914	16	US-10-437-963-131538
44	41.5	47.2	566	15	US-10-287-226-300
45	41.5	47.2	589	9	US-09-740-041-2

#### ALIGNMENTS

#### RESULT 1

US-10-036-444-5  
; Sequence 5, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036.444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-5

Query Match 100.0%; Score 88; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 9.9e-08;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLLLRAGFYAVSFLSVAVG 19

Db 1 VLLLRAGFYAVSFLSVAVG 19

#### RESULT 2

US-10-696-259-10

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; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-10

Query Match      100.0%; Score 88; DB 16; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
DB 138 VLLLRAGFYAVSFSLVAVG 156

RESULT 3
US-10-696-259-8
; Sequence 8, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-8

Query Match      100.0%; Score 88; DB 16; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
DB 137 VLLLRAGFYAVSFSLVAVG 155

RESULT 4
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-5

Query Match      100.0%; Score 88; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
DB 139 VLLLRAGFYAVSFSLVAVG 157

RESULT 5
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-696-259-7

Query Match      100.0%; Score 88; DB 16; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFSLVAVG 19
DB 137 VLLLRAGFYAVSFSLVAVG 155

RESULT 6
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
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; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US2002014244A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      100.0%; Score 88; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 7
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match      100.0%; Score 88; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 8
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      100.0%; Score 88; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 9
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      100.0%; Score 88; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VLLLRAGFYAVSFLSVAVG 19
      |||||
Db      139 VLLLRAGFYAVSFLSVAVG 157

RESULT 10
US-10-437-963-161934
; Sequence 161934, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
```

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; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 161934
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_610730.1.pep
US-10-437-963-161934

Query Match          55.7%; Score 49; DB 16          Length 100;
Best Local Similarity 57.9%; Pred. No. 2;
Matches 11; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VLLRAGFYAVSFSLSVAVG 19
Db 23 LLGVRAGFFRFSFLSEPVG 41

RESULT 11
US-10-424-599-207360
; Sequence 2, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207360
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_292710.1.pep
US-10-424-599-207360

Query Match          54.5%; Score 48; DB 15          Length 428;
Best Local Similarity 68.8%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRAGFYAVSFSLSVAVG 19
Db 122 LRAGVKSILSLSVAG 137

RESULT 12
US-10-121-393-2
; Sequence 2, Application US/10121393
; Publication No. US20030115633A1
; GENERAL INFORMATION:
; APPLICANT: Pais, Marie Salome Soares
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladje
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES RELATING TO PAPAYA RIPENING
; FILE REFERENCE: 19603/3001
; CURRENT APPLICATION NUMBER: US/10/121,393
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,008

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; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Carica papaya
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa at position 143 in this sequence is any amino
; OTHER INFORMATION: acid
US-10-121-393-2

Query Match          54.5%; Score 48; DB 14;          Length 665;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRAGFYAVSFSLSVAVG 19
Db 383 LRAGINKISILSVAVG 398

RESULT 13
US-10-121-539-2
; Sequence 2, Application US/10121539
; Publication No. US20030204869A1
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladje
; APPLICANT: Pais, Maria Salome Soares
; APPLICANT: Chiang, Chu-Hui
; TITLE OF INVENTION: A METHOD TO CONTROL THE RIPENING OF PAPAYA FRUIT AND
; TITLE OF INVENTION: CONFER DISEASE RESISTANCE TO PAPAYA PLANTS
; FILE REFERENCE: 19603/3601
; CURRENT APPLICATION NUMBER: US/10/121,539
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,022
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Carica papaya
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (143)
; OTHER INFORMATION: Xaa at position 143 in this sequence is any amino
; OTHER INFORMATION: acid
US-10-121-539-2

Query Match          54.5%; Score 48; DB 14;          Length 665;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 LRAGFYAVSFSLSVAVG 19
Db 383 LRAGINKISILSVAVG 398

RESULT 14
US-10-121-393-6
; Sequence 6, Application US/10121393
; Publication No. US20030115633A1
; GENERAL INFORMATION:
; APPLICANT: Pais, Marie Salome Soares
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladje
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES RELATING TO PAPAYA RIPENING
; FILE REFERENCE: 19603/3001
; CURRENT APPLICATION NUMBER: US/10/121,393
; CURRENT FILING DATE: 2002-04-11

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; PRIOR APPLICATION NUMBER: 60/293,008
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 721
; TYPE: prt
; ORGANISM: Carica papaya
US-10-121-393-6

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Query Match 54.5%; Score 48; DB 14; Length 721;  
Best Local Similarity 68.8%; Pred. No. 26;  
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 L R A G F Y A V S F L S V A V G 19  
||| ||| ||| : |||  
Db 526 L R A G V N K V S L L S I A V G 541

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RESULT 15
US-10-121-539-6
; Sequence 6, Application US/10121539
; Publication No. US20030204869A1
; GENERAL INFORMATION:
; APPLICANT: Gonsalves, Dennis
; APPLICANT: Balde, Aladjje
; APPLICANT: Pais, Maria Salome Soares
; APPLICANT: Chiang, Chu-Hui
; TITLE OF INVENTION: A METHOD TO CONTROL THE RIPENING OF PAPAYA FRUIT AND
; TITLE OF INVENTION: CONFER DISEASE RESISTANCE TO PAPAYA PLANTS
; FILE REFERENCE: 19603/3601
; CURRENT APPLICATION NUMBER: US/10/121.539
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,022
; PRIOR FILING DATE: 2001-04-11
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Carica papaya
US-10-121-539-6

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Query Match 54.5%; Score 48; DB 14; Length 721;  
Best Local Similarity 68.8%; Pred. No. 26;  
Matches 11: Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LRAGFYAVSFLSVAVG 19  
||| ||| : |||  
Db 526 LRAGVTKVSLLSIAVG 541

Search completed: November 16, 2004, 19:45:05  
Job time : 17.9841 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:05:01 ; Search time 63.2493 Seconds  
(without alignments)  
332.841 Million cell updates/sec

Title: US-10-036-444-5

Perfect score: 88

Sequence: 1 VLLLRAGFYAVSFLSVAVG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:\*

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4: /cgn2\_6/ptodata/1/paa/US08 COMB.pcp.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	88	100.0	19	18	US-09-440-514-5	Sequence 5, Appli
2	88	100.0	19	18	US-09-456-199-5	Sequence 5, Appli
3	88	100.0	19	26	US-10-036-444-5	Sequence 5, Appli
4	88	100.0	152	22	US-09-791-537-140678	Sequence 140678,
5	88	100.0	161	19	US-09-560-855A-10	Sequence 10, Appl
6	88	100.0	161	32	US-10-696-259-10	Sequence 10, Appl
7	88	100.0	165	22	US-09-791-537-140916	Sequence 140916,
8	88	100.0	175	19	US-09-560-855A-8	Sequence 8, Appli
9	88	100.0	175	32	US-10-696-259-8	Sequence 8, Appli
10	88	100.0	176	22	US-09-791-537-141562	Sequence 141562,
11	88	100.0	177	19	US-09-560-855-5	Sequence 5, Appli
12	88	100.0	177	19	US-09-560-855A-5	Sequence 5, Appli
13	88	100.0	177	22	US-09-791-537-140612	Sequence 140612,
14	88	100.0	177	27	US-10-170-205B-32655	Sequence 32655, A
15	88	100.0	177	32	US-10-696-259-5	Sequence 5, Appli
16	88	100.0	177	36	US-60-443-566-3830	Sequence 3830, Ap
17	88	100.0	177	36	US-60-452-680-24533	Sequence 24533, A
18	88	100.0	177	36	US-60-455-444-8478	Sequence 8478, Ap
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23	88	100.0	190	18	US-09-456-199-2	Sequence 2, Appli
24	88	100.0	190	19	US-09-560-855-4	Sequence 4, Appli
25	88	100.0	190	19	US-09-560-855A-4	Sequence 4, Appli
26	88	100.0	190	26	US-10-036-444-2	Sequence 2, Appli
27	88	100.0	190	27	US-10-170-205B-32498	Sequence 32498, A
28	88	100.0	190	32	US-10-696-259-4	Sequence 4, Appli
29	88	100.0	190	36	US-60-443-566-3828	Sequence 3828, Ap
30	88	100.0	190	36	US-60-452-680-24531	Sequence 24531, A
31	88	100.0	190	36	US-60-455-444-8476	Sequence 8476, Ap
32	88	100.0	190	36	US-60-465-241-8476	Sequence 8476, Ap
33	88	100.0	198	19	US-09-560-855A-9	Sequence 9, Appli
34	88	100.0	198	32	US-10-696-259-9	Sequence 9, Appli
35	88	100.0	199	36	US-60-242-679-1473	Sequence 1473, Ap
36	88	100.0	201	19	US-09-560-855-6	Sequence 6, Appli
37	88	100.0	201	19	US-09-560-855A-6	Sequence 6, Appli
38	88	100.0	201	22	US-09-791-537-140989	Sequence 140989,
39	88	100.0	201	27	US-10-170-205B-32497	Sequence 32497, A
40	88	100.0	201	32	US-10-696-259-6	Sequence 6, Appli
41	88	100.0	201	36	US-60-443-566-3829	Sequence 3829, Ap
42	88	100.0	201	36	US-60-452-680-24532	Sequence 24532, A
43	88	100.0	201	36	US-60-455-444-8477	Sequence 8477, Ap
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45	88	100.0	231	22	US-09-760-476-1763	Sequence 1763, Ap

#### ALIGNMENTS

#### RESULT 1

US-09-440-514-5  
; Sequence 5, Application US/09440514  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; APPLICANT: UNIVERSITA DI GENOVA  
; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/09440514  
; CURRENT FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Human NK cell

## US-09-440-514-5

Query Match 100.0%; Score 88; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19  
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 Db 1 VLLLRAGFYAVSFLSVAVG 19

## RESULT 2

US-09-456-199-5  
 ; Sequence 5, Application US/09456199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNATE PHARMA S.A.S.  
 ; APPLICANT: UNIVERSITA DI GENOVA  
 ; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
 ; TITLE OF INVENTION: antibodies that identify the same"  
 ; FILE REFERENCE: SEQ-FR-1060  
 ; CURRENT APPLICATION NUMBER: US/09/456.199  
 ; CURRENT FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Human NK cell  
 US-09-456-199-5

Query Match 100.0%; Score 88; DB 18; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19  
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 Db 1 VLLLRAGFYAVSFLSVAVG 19

## RESULT 3

US-10-036-444-5  
 ; Sequence 5, Application US/10036444  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INNATE PHARMA S.A.S.  
 ; APPLICANT: UNIVERSITA DI GENOVA  
 ; TITLE OF INVENTION: "Novel triggering receptor involved in natural  
 ; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
 ; TITLE OF INVENTION: antibodies that identify the same"  
 ; FILE REFERENCE: SEQ-FR-1060  
 ; CURRENT APPLICATION NUMBER: US/10/036.444  
 ; CURRENT FILING DATE: 2002-01-07  
 ; PRIOR APPLICATION NUMBER: 09/440.514  
 ; PRIOR FILING DATE: 1999-11-15  
 ; PRIOR APPLICATION NUMBER: 09/456.199  
 ; PRIOR FILING DATE: 1999-12-07  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 19  
 ; TYPE: PRT  
 ; ORGANISM: Human NK cell  
 US-10-036-444-5

Query Match 100.0%; Score 88; DB 26; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-06;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19  
 |||||  
 Db 1 VLLLRAGFYAVSFLSVAVG 19

## RESULT 4

US-09-791-537-140678  
 ; Sequence 140678, Application US/09791537  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bionomix, Inc.  
 ; APPLICANT: Debe, Derek  
 ; APPLICANT: Danzer, Joseph  
 ; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
 ; TITLE OF INVENTION: METHODS OF USE THEREOF  
 ; FILE REFERENCE: 261/210  
 ; CURRENT APPLICATION NUMBER: US/09/791.537  
 ; CURRENT FILING DATE: 2001-02-22  
 ; NUMBER OF SEQ ID NOS: 153055  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 140678  
 ; LENGTH: 152  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-791-537-140678

Query Match 100.0%; Score 88; DB 22; Length 152;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19  
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 Db 114 VLLLRAGFYAVSFLSVAVG 132

## RESULT 5

US-09-560-855A-10  
 ; Sequence 10, Application US/09560855A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOGEN, INC  
 ; APPLICANT: BROWNING, Jeffrey  
 ; TITLE OF INVENTION: EMOG, A Novel Protein Member of the  
 ; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
 ; TITLE OF INVENTION: Immunomodulatory Purposes  
 ; FILE REFERENCE: A041 US  
 ; CURRENT APPLICATION NUMBER: US/09/560.855A  
 ; CURRENT FILING DATE: 2000-04-28  
 ; PRIOR APPLICATION NUMBER: PCT/US98/23826  
 ; PRIOR FILING DATE: 1998-11-05  
 ; PRIOR APPLICATION NUMBER: 60/064761  
 ; PRIOR FILING DATE: 1997-11-07  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 10  
 ; LENGTH: 161  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 US-09-560-855A-10

Query Match 100.0%; Score 88; DB 19; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 4e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFLSVAVG 19  
 |||||  
 Db 138 VLLLRAGFYAVSFLSVAVG 156

## RESULT 6

US-10-696-259-10  
 ; Sequence 10, Application US/10696259  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BIOGEN, INC  
 ; APPLICANT: BROWNING, Jeffrey  
 ; TITLE OF INVENTION: EMOG, A Novel Protein Member of the  
 ; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
 ; TITLE OF INVENTION: Immunomodulatory Purposes  
 ; FILE REFERENCE: A041 US  
 ; CURRENT APPLICATION NUMBER: US/10/696.259



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; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-696-259-10
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Query Match 100.0%; Score 88; DB 32; Length 161;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
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Db 138 VLLLRAGFYAVSFLSVAVG 156
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RESULT 7
US-09-791-537-140916
; Sequence 140916, Application US/09/791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: MYELIN-OLIGODENDROCYTE GLYCOPROTEIN FAMILY AND ITS USE FOR
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140916
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-140916
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Query Match 100.0%; Score 88; DB 22; Length 165;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
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Db 114 VLLLRAGFYAVSFLSVAVG 132
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RESULT 8
US-09-560-855A-8
; Sequence 8, Application US/09560855A
; GENERAL INFORMATION:
; APPLICANT: BIONOMIX, INC.
; APPLICANT: BROWNING, JEFFREY
; TITLE OF INVENTION: BMOG, A NOVEL PROTEIN MEMBER OF THE
; TITLE OF INVENTION: MYELIN-OLIGODENDROCYTE GLYCOPROTEIN FAMILY AND ITS USE FOR
; TITLE OF INVENTION: IMMUNOMODULATORY PURPOSES
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/09/560,855A
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-560-855A-8
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Query Match 100.0%; Score 88; DB 19; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 137 VLLLRAGFYAVSFLSVAVG 155
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RESULT 9
US-10-696-259-8
; Sequence 8, Application US/10696259
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: BROWNING, JEFFREY
; TITLE OF INVENTION: BMOG, A NOVEL PROTEIN MEMBER OF THE
; TITLE OF INVENTION: MYELIN-OLIGODENDROCYTE GLYCOPROTEIN FAMILY AND ITS USE FOR
; TITLE OF INVENTION: IMMUNOMODULATORY PURPOSES
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-8
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Query Match 100.0%; Score 88; DB 32; Length 175;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
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Db 137 VLLLRAGFYAVSFLSVAVG 155
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RESULT 10
US-09-791-537-141562
; Sequence 141562, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141562
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-141562
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Query Match 100.0%; Score 88; DB 22; Length 176;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VLLLRAGFYAVSFLSVAVG 19
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Db 114 VLLLRAGFYAVSFLSVAVG 132  
|||||

## RESULT 11

US-09-560-855-5  
; Sequence 5, Application US/09560855  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use  
; TITLE OF INVENTION: For Immunomodulatory Purposes  
; FILE REFERENCE: A041PCT  
; CURRENT APPLICATION NUMBER: US/09/560,855  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-560-855-5

Query Match 100.0%; Score 88; DB 19; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157

## RESULT 12

US-09-560-855A-5  
; Sequence 5, Application US/09560855A  
; GENERAL INFORMATION:  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/09/560,855A  
; CURRENT FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-560-855A-5

Query Match 100.0%; Score 88; DB 19; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
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Db 139 VLLLRAGFYAVSFLSVAVG 157

## RESULT 13

US-09-791-537-140612  
; Sequence 140612, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 140612  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-140612

Query Match 100.0%; Score 88; DB 22; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157

## RESULT 14

US-10-170-205E-32655  
; Sequence 32655, Application US/10170205E  
; GENERAL INFORMATION:  
; APPLICANT: ADAMS, Mark  
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN  
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF  
; FILE REFERENCE: CLOC1381  
; CURRENT APPLICATION NUMBER: US/10/170,205E  
; CURRENT FILING DATE: 2002-06-13  
; NUMBER OF SEQ ID NOS: 40312  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 32655  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-170-205E-32655

Query Match 100.0%; Score 88; DB 27; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLLLRAGFYAVSFLSVAVG 19  
|||||

Db 139 VLLLRAGFYAVSFLSVAVG 157

## RESULT 15

US-10-696-259-5  
; Sequence 5, Application US/10696259  
; GENERAL INFORMATION:  
; APPLICANT: BROWNING, Jeffrey  
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the  
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for  
; TITLE OF INVENTION: Immunomodulatory Purposes  
; FILE REFERENCE: A041 US  
; CURRENT APPLICATION NUMBER: US/10/696,259  
; CURRENT FILING DATE: 2003-10-28  
; PRIOR APPLICATION NUMBER: US/09/560,855A  
; PRIOR FILING DATE: 2000-04-28  
; PRIOR APPLICATION NUMBER: PCT/US98/23826  
; PRIOR FILING DATE: 1998-11-05  
; PRIOR APPLICATION NUMBER: 60/064761  
; PRIOR FILING DATE: 1997-11-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 177  
; TYPE: PRT

; ORGANISM: Homo sapien  
US-10-696-259-5

Query Match 100.0%; Score 88; DB 32; Length 177;  
Best Local Similarity 100.0%; Pred. No. 4.3e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLLLRAGFYAVSFSLVAVG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 139 VLLLRAGFYAVSFSLVAVG 157

Search completed: November 16, 2004, 19:38:44  
Job time : 63.2493 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 6.82759 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 791\*

1: PIR1\*

2: PIR2\*

3: PIR3\*

4: PIR4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	29.4	1801	1 MMRTS	laminin beta-2 cha
2	59.5	29.2	660	1 QMBE3	BHLPI protein - hu
3	59	28.9	544	2 T36545	probable large int
4	58.5	28.7	116	2 T46473	hypothetical prote
5	58	28.4	180	2 E84768	hypothetical prote
6	57	27.9	435	2 S40993	hypothetical prote
7	56.5	27.7	1321	2 JE0352	mucin MUC5B, trac
8	55	27.0	1620	2 T27283	hypothetical prote
9	54.5	26.7	147	2 S37485	gene msgl protein
10	54.5	26.7	3078	2 T37485	variant-specific s
11	53.5	26.5	1300	2 A36302	insulin receptor-r
12	53.5	26.2	2767	1 UIHU	thyroglobulin prec
13	53	26.0	460	2 D97679	argininosuccinate
14	53	26.0	597	2 T16006	protein kinase C3
15	52.5	25.7	91	2 S37486	gene msg3 protein
16	52.5	25.7	153	2 PN0564	von Willebrand fac
17	52.5	25.7	577	2 B37057	integrin beta-6 ch
18	52.5	25.7	799	2 A38308	integrin beta-5 ch
19	52	25.5	137	2 A87586	hypothetical prote
20	52	25.5	1798	2 S53869	laminin beta-2 cha
21	51.5	25.2	106	2 T48808	hypothetical prote
22	51.5	25.2	138	2 B95180	Hmr heavy metal d
23	51.5	25.2	378	2 B59180	Wnt inhibitory fac
24	51.5	25.2	435	2 T48724	hypothetical prote
25	51.5	25.2	436	2 D88826	protein lin-3 limp
26	51.5	25.2	438	2 S28263	lin-3 protein prec
27	51.5	25.2	929	2 T51932	kinesin [imported]
28	51.5	25.2	1166	1 S06142	protein-tyrosine k
29	51.5	25.2	1344	2 S47412	gene P2 protein -

30 51 25.0 325 2 B43692 T2 protein - rabbi  
31 51 25.0 434 1 A35005 u-plasminogen acti  
32 50.5 24.8 106 2 B64350 hypothetical prote  
33 50.5 24.8 247 2 T50874 hypothetical cytoc  
34 50.5 24.8 515 2 T32089 hypothetical prote  
35 50.5 24.8 656 2 U32005 integrin beta-5 ch  
36 50.5 24.8 677 2 H86208 protein F22G5.26 l  
37 50.5 24.8 1111 2 T26972 hypothetical prote  
38 50.5 24.8 1722 2 E89753 protein filic7.4 [i  
39 50 24.5 82 2 F68870 hypothetical prote  
40 50 24.5 174 2 C48583 stress-inducible p  
41 50 24.5 354 2 T22274 hypothetical prote  
42 50 24.5 732 2 I52361 testicular metallo  
43 50 24.5 5376 2 T42215 zonadhesin - mouse  
44 49.5 24.3 1574 2 T13954 MEGF6 protein - ra  
45 49.5 24.3 1914 2 T42635 tenascin V precurs

#### ALIGNMENTS

##### RESULT 1

##### MMRTS

laminin beta-2 chain precursor - rat

N:Alternate names: laminin chain B3; S-laminin

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 09-Jul-2004

C:Accession: S03539

R:Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.

Nature 338, 229-234, 1989

A:Title: A laminin-like adhesive protein concentrated in the synaptic cleft of the neur

A:Reference number: S03539; MUID:89159410; PMID:2922051

A:Accession: S03539

A:Molecule type: mRNA

A:Residues: 1-1801 <HUN>

A:Cross-references: UNIPROT:P15800; EMBL:X16563; NID:G57250; PIDN:CAA34561.1; PID:G5725

C:Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin

C:Function:

A:Description: interact with cells and with other basement membrane proteins to promote

C:Superfamily: laminin beta-1 chain; laminin-type EGF-like homology

C:Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-1801/Product: laminin beta-2 chain #status predicted <MAT>

F:36-285/Domain: VI <DOM6>

F:286-555/Domain: V <DOM5>

F:286-347/Domain: laminin-type EGF-like homology <LE01>

F:350-410/Domain: laminin-type EGF-like homology <LE02>

F:413-470/Domain: laminin-type EGF-like homology <LE03>

F:473-522/Domain: laminin-type EGF-like homology <LE04>

F:525-555/Domain: laminin-type EGF-like homology #status atypical <LE05>

F:556-784/Domain: IV <DOM4>

F:786-831/Domain: laminin-type EGF-like homology <LE06>

F:788-1156/Domain: III <DOM3>

F:834-877/Domain: laminin-type EGF-like homology <LE07>

F:880-927/Domain: laminin-type EGF-like homology <LE08>

F:930-986/Domain: laminin-type EGF-like homology <LE09>

F:989-1038/Domain: laminin-type EGF-like homology <LE10>

F:1041-1095/Domain: laminin-type EGF-like homology <LE11>

F:1098-1143/Domain: laminin-type EGF-like homology <LE12>

F:1146-1190/Domain: laminin-type EGF-like homology <LE13>

F:1197-1412/Domain: II <DOM2>

F:1197-1412/Region: heptad repeats

F:1413-1445/Domain: alpha <ALP>

F:1446-1801/Region: heptad repeats

F:1446-1801/Domain: I <DOM1>

F:45-50/Disulfide bonds: #status predicted

F:251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status 1

F:193,1196,1800/Disulfide bonds: interchain #status predicted

Query Match 29.4%; Score 60; DB 1; Length 1801;

Best Local Similarity 29.8%; Pred. No. 21;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;



JE0352  
mucin MUC5B, tracheobronchial - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 21-Jul-2000  
C:Accession: JE0352  
R:Offner, G.D.; Nunes, D.P.; Keates, A.C.; Afdhal, N.H.; Troxler, R.F.  
Biochem. Biophys. Res. Commun. 251, 350-355, 1998  
A:Title: The amino-terminal sequence of MUC5B contains conserved multifunctional D domain  
A:Reference number: JE0352; MUID:99009274; PMID:9790959  
A:Accession: JE0352  
A:Molecule type: mRNA  
A:Residues: 1-1321 <OFF>  
A:Cross-references: GB:AF086604; NID:g3789926; PIDN:AAC67545.1; PID:g3789927  
C:Comment: This protein is large multimeric glycoproteins which is secreted by epithelial  
C:Genetics:  
A:Gene: MUC5B

Query Match 27.7%; Score 56.5; DB 2; Length 1321;  
Best Local Similarity 39.0%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 10; Indels 15; Gaps 3;

QY 7 GKCH-----CHMGTHCHS-----SDGPRGVPEPRCP 33  
Db 816 GSCHTLDVGC-FSTHCVSGVCVCPPLVSDGSGGCIABEDCP 855

RESULT 8  
T27283  
hypothetical protein Y64G10A.f - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T27283  
R:Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A:Reference number: Z20336  
A:Accession: T27283  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1620 <WIL>  
A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CA854471.1; CESP:Y64G10A.f  
A:Experimental source: clone Y64G10A  
C:Genetics:  
A:Gene: CESP:Y64G10A.f  
A:Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match 27.0%; Score 55; DB 2; Length 1620;  
Best Local Similarity 46.2%; Pred. No. 78;  
Matches 12; Conservative 0; Mismatches 8; Indels 6; Gaps 1;

QY 8 KCHCHMGTHCHSSDGRGVPEPRCP 33  
Db 1012 KCCADGMHCDPSDG-----ECICP 1031

RESULT 9  
S37485  
gene msg1 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: I48669; S37485  
R:Tromlik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.  
Gene 142, 175-182, 1994  
A:Title: Three novel SMK1-related cDNAs characterized in the submaxillary gland of mice  
A:Reference number: I48669; MUID:94252564; PMID:8194749  
A:Accession: I48669  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-147 <RES>  
A:Cross-references: UNIPROT:Q61900; EMBL:X71629; NID:g406256; PIDN:CAA50836.1; PID:g4062  
C:Genetics:  
A:Gene: msg1  
C:Superfamily: proline-rich peptide P-B

Query Match 26.7%; Score 54.5; DB 2; Length 147;  
Best Local Similarity 44.0%; Pred. No. 10;  
Matches 11; Conservative 0; Mismatches 11; Indels 3; Gaps 1;

QY 9 CHCHMGTHCHSSDGRGVPEPRCP 33  
Db 20 CECHGRPRHD---PRGFFPPPPP 41

RESULT 10  
T28432  
variant-specific surface protein 1 - malaria parasite (Plasmodium falciparum)  
N:Alternate names: erythrocyte membrane binding protein 1 (EMBL)  
C:Species: Plasmodium falciparum  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T28432  
R:Su, X.Z.; Heatwole, V.M.; Wertheimer, S.P.; Guinet, F.; Herrfeldt, J.A.; Peterson, D.; Cell 82, 89-100, 1995  
A:Title: The large diverse gene family var encodes proteins involved in cytoadherence a  
A:Reference number: Z20487; MUID:95330613; PMID:7606788  
A:Accession: T28432  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-3078 <SUX>  
A:Cross-references: UNIPROT:Q26031; EMBL:L40608; NID:g886374; PID:g886375; PIDN:AAA7539  
C:Genetics:  
A:Gene: var-1  
A:Introns: 2611/3

Query Match 26.7%; Score 54.5; DB 2; Length 3078;  
Best Local Similarity 40.0%; Pred. No. 1.6e+02;  
Matches 12; Conservative 2; Mismatches 15; Indels 1; Gaps 1;

QY 5 YQKCHCHMGTHCHS-SDGPRGVPEPRCP 33  
Db 1698 YPEKCDYQGHVPSIPPPPPVQFQPEAP 1727

RESULT 11  
A36502  
insulin receptor-related receptor precursor - guinea pig  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 01-Feb-1991 #sequence\_revision 01-Feb-1991 #text\_change 09-Jul-2004  
C:Accession: A36502  
R:Shier, P.; Watt, V.M.  
J. Biol. Chem. 264, 14605-14608, 1989  
A:Title: Primary structure of a putative receptor for a ligand of the insulin family.  
A:Reference number: A36502; MUID:89359245; PMID:2768234  
A:Accession: A36502  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1300 <SHI>  
A:Cross-references: UNIPROT:P14617; GB:J05047  
C:Superfamily: insulin receptor; protein kinase homology  
C:Keywords: ATP; autophosphorylation; phosphoprotein; receptor; transmembrane protein  
F:977-1253/Domain: protein kinase homology <KIN>  
F:985-993/Region: protein kinase ATP-binding motif

Query Match 26.5%; Score 54; DB 2; Length 1300;  
Best Local Similarity 52.6%; Pred. No. 85;  
Matches 10; Conservative 2; Mismatches 5; Indels 2; Gaps 1;

QY 4 YYQKCH-CHMGTHCHS 20  
Db 253 YYQSACHRACPLGTVEHS 271

RESULT 12  
U1HU  
thyroglobulin precursor, major splice form - human  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1986 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: A59110; S00014; A01532; S03422; I38343; I57669; S02266; S39432; S66241; S6

R;Malthiery, Y.  
 Submitted to the EMBL Data Library, April 1988  
 A:Description: Human mRNA for thyroglobulin.  
 A:Reference number: A59110  
 A:Accession: A59110  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-2767 <MAL1>  
 A:Cross-references: UNIPROT:P01266; UNIPROT-Q15948; GB:X05615; NID:G37173; PIDN:CAA29104  
 A:Note: revision to S00014  
 R;Malthiery, Y.; Lissitzky, S.  
 Eur. J. Biochem. 165, 491-498, 1987  
 A:Title: Primary structure of human thyroglobulin deduced from the sequence of its 8448-  
 A:Reference number: S00014; MUID:87246630; PMID:3595599  
 A:Accession: S00014  
 A:Molecule type: mRNA  
 A:Residues: 1-1041, 'Y', 1043-1057, 'T', 1059-2767 <MAL2>  
 A:Cross-references: GB:X05615; NID:G37173  
 A:Note: this sequence is revised in A59110  
 R;Malthiery, Y.; Lissitzky, S.  
 Eur. J. Biochem. 147, 53-58, 1985  
 A:Title: Sequence of the 5'-end quarter of the human-thyroglobulin messenger ribonucleic  
 A:Reference number: A01532; MUID:85127024; PMID:3971976  
 A:Accession: A01532  
 A:Molecule type: mRNA  
 A:Residues: 1-730 <MAW>  
 A:Cross-references: GB:X02154; NID:G37175; PIDN:CAA26089.1; PID:G1335349  
 A:Note: the translated sequence in GenBank entry HSTHYRRS, release 111.0, (PIDN:CAA26089  
 n 1-Met  
 R;Parma, J.; Christophe, D.; Pohl, V.; Vassart, G.  
 J. Mol. Biol. 196, 769-779, 1987  
 A:Title: Structural organization of the 5' region of the thyroglobulin gene. Evidence fo  
 A:Reference number: S03422; MUID:88062712; PMID:3681978  
 A:Accession: S03422  
 A:Molecule type: DNA  
 A:Residues: 1-134, 'G', 136-415, 640-652, 'G', 654-733, 'A', 735-737, 880-983, 'DR', 985-999 <PAR>  
 A:Cross-references: EMBL:X06059; NID:G37145; PIDN:CAA29454.1; PID:G1359884; EMBL:X06067;  
 R;Christophe, D.; Cabrer, B.; Bacoll, A.; Targovnik, H.; Pohl, V.; Vassart, G.  
 Nucleic Acids Res. 13, 5121-5144, 1985  
 A:Title: An unusually long poly(purine)-poly(pyrimidine) sequence is located upstream fr  
 A:Reference number: I38343; MUID:85269632; PMID:2991855  
 A:Accession: I38343  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-22, 'GKX' <CHR>  
 A:Cross-references: EMBL:X02749; NID:G37162; PIDN:CAA26527.1; PID:G758106  
 R;Targovnik, H.M.; Cochaux, P.; Corach, D.; Vassart, G.  
 Mol. Cell. Endocrinol. 84, R23-R26, 1992  
 A:Title: Identification of a minor TG mRNA transcript in RNA from normal and goitrous th  
 A:Reference number: I57669; MUID:93347597; PMID:1639210  
 A:Accession: I57669  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1503-1508, 'L', 1567-1601 <REW>  
 A:Cross-references: GB:S40807; NID:G252170; PIDN:AAB22685.1; PID:G252171  
 A:Note: this sequence fragment represents a minor splice form  
 R;Marriq, C.; Lejeune, P.J.; Venot, N.; Vinet, L.  
 FEBS Lett. 242, 414-418, 1989  
 A:Title: Hormone synthesis in human thyroglobulin: possible cleavage of the polypeptide  
 A:Reference number: S02266; MUID:8912111; PMID:2914619  
 A:Accession: S02266  
 A:Contents: evidence for Tyr-149 as ring donor for thyroxine formation  
 A:Molecule type: protein  
 A:Residues: 101-109, 114-121, 126-131, 143-149 <MAR>  
 A:Note: only the first peptide was sequenced; others were isolated and their amino acid  
 R;Gentile, F.; Salvatore, G.  
 Eur. J. Biochem. 218, 603-621, 1993  
 A:Title: Preferential sites of proteolytic cleavage of bovine, human and rat thyroglobul  
 A:Reference number: S39431; MUID:94094855; PMID:8369951  
 A:Accession: S39431  
 A:Molecule type: protein  
 A:Residues: 20-27, 522-527, 541-547, 616-619, 'X', 621, 1001-1005, 1009-1011, 'X', 1013, 1424-1430  
 R;Xiao, S.; Pollock, H.G.; Targovnik, A.; Rawitch, A.B.  
 Arch. Biochem. Biophys. 320, 96-105, 1995  
 A:Title: Characterization of hormonogenic sites in an N-terminal, cyanogen bromide fragm  
 A:Reference number: S66241; MUID:95314327; PMID:7793989  
 A:Accession: S66241  
 A:Molecule type: protein  
 A:Residues: 'D', 21-23, 45-47, 147-148, 150-152 <XIA>  
 R;Yang, S.X.; Pollock, H.G.; Rawitch, A.B.  
 Arch. Biochem. Biophys. 327, 61-70, 1996  
 A:Title: Glycosylation in human thyroglobulin: location of the N-linked oligosaccharide  
 A:Reference number: S62778; MUID:96201348; PMID:8615697  
 A:Accession: S62778  
 A:Molecule type: protein  
 A:Residues: 69-84, 196-210, 'T', 212-213, 476-492, 523-539, 741-770, 811-848, 850-853, 938-950, 12  
 6-1783, 'D', 1785, 'R', 1999-2017, 2241-2258, 2270-2285, 'P', 2287-2307, 2578-2584 <YAN>  
 R;Teiri, T.; Cochaux, P.; Targovnik, H.M.; Suzuki, M.; Shimoda, S.; Perret, J.; Vassart,  
 J. Clin. Invest. 88, 1901-1905, 1991  
 A:Title: A 3' splice site mutation in the thyroglobulin gene responsible for congenital  
 A:Reference number: I55565; MUID:92091498; PMID:1752952  
 A:Accession: I55565  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 90-91, 160-161 <JEI>  
 A:Cross-references: GB:S71821; NID:G240935; PIDN:AAB20665.1; PID:G240936  
 A:Note: mutant splice form  
 C:Comment: The thyroglobulin molecule is produced in the thyroid gland and is the precur  
 C:Genetics:  
 A:Gene: GDB:TG  
 A:Cross-references: GDB:120434; OMIM:188450  
 A:Map position: 8q24.2-8q24.3  
 A:Introns: 23/1; 59/2; 92/1; 160/1; 213/2; 249/1; 297/1; 359/1; 726/1; 921/1; 1000/1 #st  
 C:Complex: homodimer  
 C:Function:  
 A:Description: precursor of thyroid hormones thyroxine and triiodothyronine; iodine stor  
 C:Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol  
 C:Keywords: alternative splicing; duplication; glycoprotein; homodimer; iodine; thyroid  
 F:20-2767/Product: thyroglobulin #status predicted <SIG>  
 F:34-92/Domain: thyroglobulin type I repeat homology <MAT>  
 F:96-160/Domain: thyroglobulin type I repeat homology <THY1>  
 F:164-297/Domain: thyroglobulin type I repeat homology #status atypical <THY3>  
 F:301-358/Domain: thyroglobulin type I repeat homology <THY4>  
 F:608-658/Domain: thyroglobulin type I repeat homology <THY5>  
 F:662-726/Domain: thyroglobulin type I repeat homology <THY6>  
 F:730-921/Domain: thyroglobulin type I repeat homology #status atypical <THY7>  
 F:925-1072/Domain: thyroglobulin type I repeat homology #status atypical <THY8>  
 F:1076-1144/Domain: thyroglobulin type I repeat homology <THY9>  
 F:1148-1209/Domain: thyroglobulin type I repeat homology <THY10>  
 F:1455-1468/Region: type II repeat  
 F:1469-1485/Region: type II repeat  
 F:1486-1502/Region: type II repeat  
 F:1602-1722/Region: type IIIa repeat  
 F:1723-1891/Region: type IIIb repeat  
 F:1892-1994/Region: type IIIa repeat  
 F:1995-2128/Region: type IIIb repeat  
 F:2129-2186/Region: type IIIa repeat  
 F:2237-2725/Domain: cholinesterase homology <ACE>  
 F:242, 2572, 2586/Modified site: thyroxine (Tyr) #status predicted  
 F:76, 198, 484, 529, 748, 816, 947, 1219, 1348, 1364, 1715, 1773, 2012, 2249, 2294, 2581/Binding site:  
 F:110, 496, 1868, 2121/Binding site: carbohydrate (Asn) (covalent) #status absent  
 F:149/Modified site: denhydroalanine (Tyr) #status predicted  
 F:2765/Modified site: triiodothyronine (Tyr) #status predicted  
 Query Match 26.2%; Score 53.5; DB 1; Length 2767;  
 Best Local Similarity 31.2%; Pred. No. 1.9e+02;  
 Matches 15; Conservative 2; Mismatches 12; Indels 19; Gaps 3;  
 QY 5 YQKGC-----HCHMGT-HCHSSDGRGVPE-----PRCP 33  
 DB 1026 YMQCDAFGSWEPEVQCHAGTGHCVDEKGFPGSLTARSLQIPQCP 1073  
 RESULT 13  
 D37679



argininosuccinate synthase (PA3525) [imported] - Agrobacterium tumefaciens (strain C59,  
C:Species: Agrobacterium tumefaciens  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
C:Accession: D97879  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markels, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: D97879  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-460 <KUR>  
A:Cross-references: GB:AE007869; PIDN:AAK88389.1; PID:G15157878; GSPDB:GN00169  
C:Genetics:  
A:Gene: AGR C 4936  
A:Map position: circular chromosome  
C:Superfamily: argininosuccinate synthase

Query Match 26.0%; Score 53; DB 2; Length 460;  
Best Local Similarity 40.0%; Pred. No. 44;  
Matches 12; Conservative 3; Mismatches 11; Indels 4; Gaps 1;  
QY 4 YYQGGKCHCHMGTHCHSSDGRGVIPRCP 33  
DB 18 YLTKRRTTHFLGLCKSAEIPR----KWRCP 43

RESULT 14  
T16006  
Protein kinase C3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: T16006; T37253  
R:Chisoe, S.  
submitted to the EMBL Data Library, September 1995  
A:Description: The sequence of C. elegans cosmid F09E5.  
A:Reference number: Z1844  
A:Accession: T16006  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-597 <CHI>  
A:Cross-references: UNIPROT:Q19266; EMBL:U37429; NID:G1019949; PID:G1019950; PIDN:AAA793  
A:Experimental source: strain Bristol N2  
R:Wu, S.L.; Rubin, C.S.  
submitted to the EMBL Data Library, September 1997  
A:Description: Molecular characterization of an atypical protein kinase C from C. elegans  
A:Reference number: Z21647  
A:Accession: T37253  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-597 <WUS>  
A:Cross-references: EMBL:AF025666; PIDN:AAB88885.1  
A:Experimental source: strain Bristol N2  
C:Genetics:  
A:Gene: F09E5.1; pkC-3  
A:Map position: II  
A:Introns: 22/3; 109/1; 137/2; 179/3; 238/3; 322/3; 442/2; 556/3  
C:Superfamily: protein kinase C, zeta/iota type; protein kinase C zinc-binding repeat ho  
F:128-177/Domain: protein kinase C zinc-binding repeat homology <KZN>  
F:251-522/Domain: protein kinase homology <KIN>

Query Match 26.0%; Score 53; DB 2; Length 597;  
Best Local Similarity 50.0%; Pred. No. 56;  
Matches 11; Conservative 3; Mismatches 6; Indels 2; Gaps 2;  
QY 8 KCHCHMGTHC-HSSDGRGVIP 28  
DB 168 KCHRHVTHCGQALQGP-NIIP 188

RESULT 15  
S37486

gene msg3 protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: I48671; S37486  
R:Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.  
Gene 142, 175-182, 1994  
A:Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mice  
A:Reference number: I48669; MUID:94252564; PMID:8194749  
A:Accession: I48671  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-91 <RES>  
A:Cross-references: UNIPROT:Q61902; EMBL:X71631; NID:G406260; PIDN:CAAS0638.1; PID:G406  
C:Genetics:  
A:Gene: msg3  
C:Superfamily: proline-rich peptide P-B

Query Match 25.7%; Score 52.5; DB 2; Length 91;  
Best Local Similarity 45.5%; Pred. No. 12;  
Matches 10; Conservative 0; Mismatches 9; Indels 3; Gaps 1;  
QY 9 CHCHMGTHCHSSDGRGVIP 30  
DB 20 CECHRGPRRH---PRGPFPPP 38

Search completed: November 16, 2004, 19:15:56  
Job time : 8.82759 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 36.8515 seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-6  
Perfect score: 204  
Sequence: 1 STVYQKCHGMTHCHSSDGRGVIPEPRCP 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.4

1: uniprot\_sprot.4

2: uniprot\_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	142	69.6	180	1 NCT3_MACMU	Q8mj02 macaca mula
2	119	58.3	176	1 NCT3_MACFA	P61483 macaca fasc
3	67	32.8	192	1 NCT3_RAT	Q8cf09 rattus norv
4	63.5	31.1	665	2 Q7VZW9	Q7vzw9 bordetella
5	63.5	31.1	665	2 Q7WLN6	Q7wln6 bordetella
6	63.5	31.1	665	2 Q7WQ11	Q7wq11 bordetella
7	61	29.9	485	2 Q97271	Q97271 plasmodium
8	60	29.4	201	1 NCT3_HUMAN	O14931 homo sapien
9	60	29.4	201	1 NCT3_PANTR	P61484 pan troglod
10	60	29.4	371	2 Q7RC43	Q7rc43 plasmodium
11	60	29.4	1799	1 LMB2_MOUSE	Q61292 mus musculu
12	60	29.4	1799	2 Q8R0Y0	Q8r0y0 mus musculu
13	60	29.4	1801	1 LMB2_RAT	P15800 rattus norv
14	59.5	29.2	660	1 VHL1_EBV	P03181 epstein-bar
15	59.5	29.2	660	2 Q77733	Q77733 human herpe
16	59.5	29.2	660	2 CAD53473	Cad53473 human her
17	59.5	29.2	3170	2 Q7FNS0	Q7fn80 anopheles g
18	59	28.9	544	2 Q9X822	Q9x822 streptomyce
19	58.5	28.7	116	2 Q9NT74	Q9nt74 homo sapien
20	58.5	28.7	2471	1 NTC2_HUMAN	Q04721 homo sapien
21	58	28.4	180	2 Q82257	Q82257 arabidopsis
22	58	28.4	845	1 AD09_MOUSE	Q51072 mus musculu
23	57.5	28.2	198	2 Q90030	Q90030 human herpe
24	57.5	28.2	881	2 Q9W0A0	Q9w0a0 drosophila
25	56.5	27.7	969	2 Q96K96	Q96k96 homo sapien
26	56.5	27.7	1140	2 Q80T91	Q80t91 mus musculu
27	56	27.5	131	2 Q6IK23	Q6ik23 drosophila
28	55.5	27.2	117	2 Q6SMW9	Q6smw9 human cytom
29	55.5	27.2	117	2 AAR31547	Aar31547 human cyt
30	55.5	27.2	1140	2 Q36KG7	Q36kg7 homo sapien
31	55.5	27.2	1147	2 Q6DIB5	Q6dib5 mus musculu

#### ALIGNMENTS

##### RESULT 1

##### NCT3\_MACMU

ID NCT3\_MACMU STANDARD; PRT; 180 AA.  
AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
DE cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.  
OC Ceropithecinae; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
RA LaBonte M.L., Miller J., Letvin N.L.;  
RT "Molecular cloning of rhesus monkey NKP46 and NKP30 and identification of NKP46SD and NKP30S.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.  
RN [2]  
SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
RC TISSUE=Lymphoid;  
RA Rizzi M., Biassoni R.;  
RT "NCR expressed by macaca NK cells.";  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q8MJ02-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
CC Note=No experimental confirmation available;  
CC Name=4;  
CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
CC Note=No experimental confirmation available;  
CC Name=5;  
CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
-----  
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32 55.5 27.2 2931 2 Q9W2C6 Q9w2c6 drosophila  
33 55.5 27.2 2968 2 Q8MLU9 Q8mlu9 drosophila  
34 55.5 27.2 2968 2 AAM71018 Aam71018 drosophila  
35 55 27.0 178 2 Q6P750 Q6p750 rattus norv  
36 55 27.0 178 2 AAM61833 Aam61833 rattus norv  
37 55 27.0 299 2 Q6GQ38 Q6gq38 xenopus lae  
38 55 27.0 744 2 Q7Q7D9 Q7q7d9 anopheles g  
39 55 27.0 1664 2 Q8TVQ2 Q8tvq2 caenorhabdi  
40 54.5 26.7 144 2 Q8DJ62 Q8dj62 synechococc  
41 54.5 26.7 147 1 SMX1\_MOUSE Q6nyu6 aspergillus  
42 54.5 26.7 680 2 Q8MYU6 Q8myu6 aspergillus  
43 54.5 26.7 680 2 CAE47913 Cae47913 aspergill  
44 54.5 26.7 814 2 Q6ZJW8 Q6zjw8 homo sapien  
45 54.5 26.7 814 2 BAC85504 Bac85504 homo sapi

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CC -----
CC EMBL; AY035214; AAKG31116.1; -
CC EMBL; AY035215; AAKG31117.1; -
CC EMBL; AY035216; AAKG31118.1; -
CC EMBL; AY035217; AAKG31119.1; -
CC EMBL; AJ554301; CAD86942.1; -
CC HSP; P16410; I185.
CC InterPro; IPR003599; IG.
CC Pfam; PF00047; IG; 1.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Alternative splicing; Glycoprotein; Immunoglobulin domain;
KW Polymorphism; Receptor; Signal; Transmembrane.
FT SIGNAL 1 18
FT CHAIN 19 180
FT DOMAIN 19 133
FT TRANSMEM 134 154
FT DOMAIN 155 180
FT DOMAIN 159 126
FT DISULFID 39 108
FT CARBOHYD 42 42
FT CARBOHYD 121 121
FT VARSPPLIC 66 90
FT VARSPPLIC 112 115
FT VARSPPLIC 116 180
FT VARSPPLIC 177 180
FT VARIANT 156 156
FT SEQUENCE 180 AA; 19639 MW; 52DF53487B2A3B6 CRC64;
Query Match 69.6%; Score 142; DB 1; Length 180;
Best Local Similarity 95.7%; Pred. No. 4.8e-10;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGP 23
Db 158 STLYYQKCHCHMGTHCHSSDGP 180

RESULT 2
NCT3 MACFA STANDARD; PRT; 176 AA.
AC P61483; Q95JB8;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer
DE cell p30-related protein) (NKP30) (NK-p30).
GN Name=NCR3; Synonyms=IC7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Rizzi M., Biassoni R.;
RT Macaca fascicularis lymphoid cells.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -----
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).

```

RA Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J., Scherer S., Scott G., Worley D., Worley K.C., Burch P.E., Okunou G., Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G., Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G., Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Fierreira S., Foster C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T., Pfannkuch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T., Smith D., Lee H.M., Gustafson E., Cahill P., Kana A., Douchette-Stamm L., Weinstock K., Feuchel K., Weiss R.B., Dunn D.M., Green E.D., Blakeley R.W., Bouffard G.G., De Jong P.J., Osoegawa K., Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S., Krzywinski M., Machevson C., Siddiqui A., Wye N., McPherson J., Zhao S., Fraser C.M., Shetty J.J., Shatman S., Geer K., Chen Y., Abramson S., Niernan W.C., Havlak P.H., Chen R., Durbin K.J., Egan A., Ren Y., Song X.Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J., D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.D., Jackson A.R., Kalafatis K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A., Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E., Birney E., Mongin E., Ureta-Vidal A., Woodward C., Zdobnov E., Bork P., Suyama M., Torrents D., Alexandersson M., Traak B.J., Young J.M., Huang H., Wang H., King H., Daniels S., Gietzen D., Schmidt J., Stevens K., Vitt U., Wingrove J., Canara F., Mar Alba M., Abril J.P., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O., Poliakov A., Hubner N., Ganten D., Goesele C., Hummel O., Kreitler T., Lee Y.A., Monti J., Schulz H., Zimdahl H., Himmelbauer H., Lehrach H., Jacob H.J., Bronberg S., Gullings-Handley J., Jensen-Seaman M.I., Wittek A.E., Lazar J., Basko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M., Rice S., Goodstadt L., Beaton S.A., Ems R.D., Winter E.E., Webber C., Brandt P., Nyakatura G., Chakrabarti K., Chatterji S., Dewey C., Pachter D., Bray N., Yap V.B., Caspi A., Tesler G., Fevner P.A., Haussler D., Roskin K.M., Baerbach R., Clawson H., Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R., Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M., Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Rietman H., Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S., Collins F., RT "genome sequence of the Brown Norway rat yields insights into mammalian evolution." NL Nature 428:493-521(2004). [4] RP IDENTIFICATION. RX PubMed=15060004; DOI=10.1101/gr.1987704; RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shina T., RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.; RT "The genomic sequence and comparative analysis of the rat major histocompatibility complex." NL Genome Res. 14:631-639(2004). CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity). CC CC -1- SUBUNIT: Interacts with CD32 (By similarity). CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential). CC CC -1- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family. CC CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain. CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)). CC ----- EMBL; AJ430418; CAD23066.1; - DR EMBL; AJ430419; CAD23067.2; - DR EMBL; AJ430420; CAD23067.2; JOINED. DR EMBL; AY273824; AAP13457.1; -

DR EMBL; EX883046; CAB84000.1; - DR HSSP; P09793; IDQT. DR RGD; 727881; 1C7. DR InterPro; IPR003599; IG. DR InterPro; IPR007110; IG-like. DR Pfam; PF00047; IG; 1. DR SMART; SM00409; IG; 1. DR PROSITE; PS00835; IG LIKE; 1. KW Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal; Transmembrane. FT SIGNAL 1 18 Potential. FT CHAIN 19 192 Natural cytotoxicity triggering receptor 3. FT DOMAIN 19 147 Extracellular (Potential). FT TRANSMEM 148 168 Potential. FT DOMAIN 169 192 Cytoplasmic (Potential). FT DOMAIN 19 126 Ig-like. FT DISULFID 39 108 By similarity. FT VARIANT 7 7 I -> V. FT VARIANT 19 19 I -> V. FT VARIANT 82 82 A -> V. FT VARIANT 138 138 A -> T. FT CONFLICT 135 135 A -> V (in Ref. 2). SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB25D22377 CRC64; Query Match 32.8%; Score 67; DB 1; Length 192; Best Local Similarity 71.4%; Pred. No. 1.5; Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0; QY 1 STVYQKCHCHMG 14 ID Q7VZW9 PRELIMINARY; PRT; 665 AA. AC Q7VZW9; DT 01-OCT-2003 (TrEMBLrel. 25, Created) DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) DE Hydatonin utilization protein B. GN Name-hyB; OrderedLocNames=BP0754; OS Bordetella pertussis. OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; OC Alcaligenaceae; Bordetella. OX NCBI\_TaxID=520; RN [1]\_ RP SEQUENCE FROM N.A. ATCC BAA-589 / NCTC 13251; RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251; RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227; RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., RA Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., RA Felwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., RA Leather S., Meule S., Norberczak H., O'Neill S., Ormond D., Price C., RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., RA Unwin L., Whitehead S., Barrall B.G., Maskell D.J.; RA "Comparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica." RL Nat. Genet. 35:32-40(2003). DR EMBL; BX640413; CAE41060.1; - DR GO; GO:0003824; F: catalytic activity; IEA. DR InterPro; IPR005479; Cph synth L D2. DR InterPro; IPR003692; Hydatoninase B. DR Pfam; PF02538; Hydatoninase B; 1. DR PROSITE; PS00867; CPSASE\_2; UNKNOWN\_1. DR Complete proteome. KW SEQUENCE 665 AA; 72395 MW; F27204349A190508 CRC64;



RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;  
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."  
RL Nature 419:527-531(2002).  
DR EMBL: AL034556; CAB38982.3; -;  
DR InterPro: IPR000345; CytC\_heme\_BS.  
DR PROSITE: PS00190; CYTOCHROME\_C; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 485 AA; 57072 MW; 59C4467FC026C472 CRC64;  
Query Match 29.9%; Score 61; DB 2; Length 485;  
Best Local Similarity 25.0%; Pred. No. 21;  
Matches 11; Conservative 10; Mismatches 7; Indels 16; Gaps 2;  
Qy 4 YQCKKCH-----CHMGTHC-----HSDGGRGVIPPEPR 31  
Db 156 HHKGRCSFKYEWTRGCHLGRFCFCHDQSHVPEGRVVPNQ 199  
RESULT 8  
ID NCT3\_HUMAN STANDARD; PRT; 201 AA.  
AC O14931; O14930; O14932; O95667; O95668; O95669;  
DT 05-JUL-2004 (Rel. 44, Created)  
DD 05-JUL-2004 (Rel. 44, Last sequence update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer  
DE cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3; Synonyms=IC7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH  
RP CD3z, AND FUNCTION.  
RC Tissue=Lymphoid;  
RX PubMed=10562324;  
RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R.,  
RA Morelli L., Marcenaro E., Accame L., Malaepina A., Biasoni R.,  
RA Bottino C., Moretta L., Moretta A.;  
RT "Identification and molecular characterization of NKP30, a novel  
RT triggering receptor involved in natural cytotoxicity mediated by human  
RT natural killer cells."  
RL J. Exp. Med. 190:1505-1516(1999).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION  
RP WITH CD3z.  
RC Tissue=peripheral blood;  
RX Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K.,  
RA Fuji T.;  
RT "Identification of two novel single nucleotide polymorphisms in the  
RT NKP30 gene in human natural killer cells."  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
RX MEDLINE=99218514; PubMed=10202016;  
RA Neville M.J., Campbell R.D.;  
RT "A new member of the Ig superfamily and a V-ATPase G subunit are among  
RT the predicted products of novel genes close to the TNF locus in the  
RT human MHC."  
RL J. Immunol. 162:4745-4754(1999).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RC Tissue=Spleen;  
RX MEDLINE=96422187; PubMed=8824804;  
RA Nalabolu S.R., Shukla H., Nallur G., Parimoo S., Weissman S.M.;  
RT "Genes in a 220-kb region spanning the TNF cluster in human MHC."  
RL Genomics 31:215-222(1996).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX PubMed=14656967; DOI=10.1101/gr.1736803;  
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,  
RA Campbell R.D., Hood L.;  
RT "Analysis of the gene-dense major histocompatibility complex class III  
RT region and its comparison to mouse."  
RL Genome Res. 13:2621-2636(2003).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 3).  
RA Shiina S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC Tissue=Blood;  
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to  
CC the increased efficiency of activated natural killer (NK) cells to  
CC mediate tumor cell lysis.  
CC -!- SUBUNIT: Interacts with CD3z.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=6;  
CC Name=1; Synonyms=IC7a;  
CC IsoId=O14931-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2; Synonyms=IC7c;  
CC IsoId=O14931-2; Sequence=VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=3; Synonyms=IC7b;  
CC IsoId=O14931-3; Sequence=VSP\_010412;  
CC Note=No experimental confirmation available;  
CC Name=4; Synonyms=IC7e;  
CC IsoId=O14931-4; Sequence=VSP\_010411;  
CC Note=No experimental confirmation available;  
CC Name=5; Synonyms=IC7f;  
CC IsoId=O14931-5; Sequence=VSP\_010411, VSP\_010413;  
CC Note=No experimental confirmation available;  
CC Name=6; Synonyms=IC7d;  
CC IsoId=O14931-6; Sequence=VSP\_010411, VSP\_010412;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Selectively expressed by all resting and  
CC activated NK cells and weakly expressed in spleen.  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to license@sib-sib.ch).  
CC -----  
CC EMBL: AJ223153; CAB54004.1; -;  
CC EMBL: AB055881; BAB78472.1; -;





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DR InterPro: IPR000345; CytC_heme_BS.
DR PROSITE: PS00190; CYTOCHROME C; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 371 AA; 43542 MW; BC325F6C5B8D8B36 CRC64;
Query Match 29.4%; Score 60; DB 2; Length 371;
Best Local Similarity 35.7%; Pred. No. 22;
Matches 15; Conservative 5; Mismatches 6; Indels 16; Gaps 3;
QY 6 QGKCH-----CHNGTHC-----HSDGPRG---VPEPR 31
DB 145 KGTCNFCVETWTRGCHMGKFCRCHSHSHVPIGTARVWDPK 186

RESULT 11
LMB2_MOUSE
ID LMB2_MOUSE STANDARD; PRT; 1799 AA.
AC Q61232; Q62182;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Laminin beta-2 chain precursor (S-laminin) (S-LAM).
GN Names=Lamb2; Synonyms=Lams;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/J;
RX MEDLINE=96278760; PubMed=8662701;
RA Durkin M.E., Gautam M., Loechel S., Sanes J.R., Merlie J.P.,
RA Albrechtsen R., Wewer U.M.;
RT "Structural organization of the human and mouse laminin beta2 chain
RT genes, and alternative splicing at the 5' end of the human
RT transcript.";
RL J. Biol. Chem. 271:13407-13416(1996).
RN [2]
RP SEQUENCE OF 348-428 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=94319092; PubMed=8043959;
RA Aberdam D., Galliano M.F., Mattai M.-G., Ortonne J.P., Meneguzzi G.;
RT "S-laminin gene (lams) maps to F1 band of mouse chromosome 9.";
RL Mamm. Genome 5:393-394(1994).
RN [3]
RP FUNCTION.
RC STRAIN=129/J;
RX MEDLINE=95191650; PubMed=7885444;
RA Noakes P.G., Gautam M., Mudd J., Sanes J.R., Merlie J.P.;
RT "Aberrant differentiation of neuromuscular junctions in mice lacking
RT S-laminin/laminin beta 2.";
RL Nature 374:258-262(1995).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- FUNCTION: Laminin-3 (S-laminin) regulates the formation of motor
CC nerve terminals.
CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three
CC different polypeptide chains (alpha, beta, gamma), which are bound
CC to each other by disulfide bonds into a cross-shaped molecule
CC comprising one long and three short arms with globules at each
CC end. The beta-2 chain is a subunit of laminin-3 (S-laminin),
CC laminin-4 (S-merosin), and laminin-7 (KS-laminin).
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -1- TISSUE SPECIFICITY: Neuromuscular synapse and kidney glomerulus.
CC -1- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -1- DOMAIN: Domains VI and IV are globular.
CC -1- SIMILARITY: Contains 13 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 1 laminin IV domain.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.

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EMBL; U43541; AAC53535.1; -  
EMBL; U42624; AAC53535.1; JOINED.  
EMBL; X75928; AAC53532.1; -  
HSP; P02468; INPE.  
MGD; MGI-99916; Lamb2.  
InterPro: IPR006209; EGF like.  
InterPro: IPR008979; Gal\_bind\_like.  
InterPro: IPR002049; Laminin\_EGF.  
InterPro: IPR008211; Laminin\_N.  
Pfam; PF00053; Laminin\_EGF; 12.  
Pfam; PF00055; Laminin\_N; 1.  
PRINTS; PS00011; EGF\_LAMININ.  
PROSITE; PS00022; EGF\_1; 10.  
PROSITE; PS01186; EGF\_2; 2.  
PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
Basement membrane; Cell adhesion; Coiled coil; Extracellular matrix;  
KW Glycoprotein; Laminin EGF-like domain; Repeat; Signal.  
FT SIGNAL 1 35 Potential.  
FT CHAIN 36 1799 Laminin beta-2 chain.  
FT DOMAIN 36 283 Laminin N-terminal (domain VI).  
FT DOMAIN 286 349 Laminin EGF-like 1.  
FT DOMAIN 350 412 Laminin EGF-like 2.  
FT DOMAIN 413 472 Laminin EGF-like 3.  
FT DOMAIN 473 524 Laminin EGF-like 4.  
FT DOMAIN 525 555 Laminin EGF-like 5 (incomplete).  
FT DOMAIN 556 782 Laminin domain IV.  
FT DOMAIN 784 831 Laminin EGF-like 6.  
FT DOMAIN 832 877 Laminin EGF-like 7.  
FT DOMAIN 878 927 Laminin EGF-like 8.  
FT DOMAIN 928 986 Laminin EGF-like 9.  
FT DOMAIN 987 1038 Laminin EGF-like 10.  
FT DOMAIN 1039 1095 Laminin EGF-like 11.  
FT DOMAIN 1096 1143 Laminin EGF-like 12.  
FT DOMAIN 1144 1190 Laminin EGF-like 13.  
FT DOMAIN 1191 1410 Domain II.  
FT DOMAIN 1411 1443 Domain alpha.  
FT DOMAIN 1444 1799 Domain I.  
FT DOMAIN 1257 1304 Coiled coil (Potential).  
FT DOMAIN 1473 1527 Coiled coil (Potential).  
FT DOMAIN 1577 1791 Coiled coil (Potential).  
FT DISULFID 286 295 By similarity.  
FT DISULFID 288 313 By similarity.  
FT DISULFID 315 324 By similarity.  
FT DISULFID 327 347 By similarity.  
FT DISULFID 350 359 By similarity.  
FT DISULFID 352 377 By similarity.  
FT DISULFID 380 389 By similarity.  
FT DISULFID 392 410 By similarity.  
FT DISULFID 413 426 By similarity.  
FT DISULFID 415 441 By similarity.  
FT DISULFID 443 452 By similarity.  
FT DISULFID 455 470 By similarity.  
FT DISULFID 473 487 By similarity.  
FT DISULFID 475 494 By similarity.  
FT DISULFID 496 505 By similarity.  
FT DISULFID 508 522 By similarity.  
FT DISULFID 784 796 By similarity.  
FT DISULFID 786 803 By similarity.  
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FT DISULFID 832 844 By similarity.  
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FT DISULFID 853 862 By similarity.  
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FT DISULFID 878 887 By similarity.  
 FT DISULFID 880 894 By similarity.  
 FT DISULFID 897 906 By similarity.  
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 FT DISULFID 928 944 By similarity.  
 FT DISULFID 930 955 By similarity.  
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 FT DISULFID 969 984 By similarity.  
 FT DISULFID 987 1001 By similarity.  
 FT DISULFID 989 1008 By similarity.  
 FT DISULFID 1011 1020 By similarity.  
 FT DISULFID 1023 1036 By similarity.  
 FT DISULFID 1096 1108 By similarity.  
 FT DISULFID 1098 1115 By similarity.  
 FT DISULFID 1117 1126 By similarity.  
 FT DISULFID 1129 1141 By similarity.  
 FT DISULFID 1144 1156 By similarity.  
 FT DISULFID 1146 1163 By similarity.  
 FT DISULFID 1165 1174 By similarity.  
 FT DISULFID 1177 1188 By similarity.  
 FT DISULFID 1191 1191 Interchain (Probable).  
 FT DISULFID 1194 1194 Interchain (Probable).  
 FT DISULFID 1798 1798 Interchain (Probable).  
 FT CARBOHYD 251 251 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 371 371 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 1086 1086 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 1250 1250 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 1309 1309 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 1349 1349 N-linked (GlcNAc... ) (Potential).  
 FT CARBOHYD 1500 1500 N-linked (GlcNAc... ) (Potential).  
 SQ SEQUENCE 1799 AA; 196352 MW; 128967A67AEDE33 CRC64;

Query Match 29.4%; Score 60; DB 1; Length 1799;  
 Best Local Similarity 29.8%; Pred. No. 1e+02;  
 Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

OY 5 YQKCHCHM-----GTHCHSSD-GPRGVPEPRC 32  
 Db 1111 FTGQCHCHAGGRTCEQELVWGDPLQCRACDCDPRG-IDKPOC 1156

RESULT 12  
 Q8ROYO PRELIMINARY; PRT; 1799 AA.  
 ID Q8ROYO  
 AC Q8ROYO  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE Laminin, beta 2.  
 GN NamesLamb2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Mix FVB/N;  
 RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC026051; AAH26051.1; -;  
 DR HSSP; P02468; INPE.  
 DR MGD; MGI:99916; Lamb2.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR005797; Cytb\_b6\_N.  
 DR InterPro; IPR006209; EGF\_like.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR002049; Laminin\_EGF.  
 DR InterPro; IPR008211; Laminin\_N.  
 DR InterPro; IPR001211; PhospholipaseA2.  
 DR Pfam; PF00053; Laminin\_EGF; 13.  
 DR Pfam; PF00055; Laminin\_N; 1.  
 DR PRINTS; PR00011; EGFLAMININ.  
 DR SMART; SM00180; EGF\_Lam; 13.  
 DR SMART; SM00136; LamNT; 1.  
 DR PROSITE; PS00192; CYTOCHROME\_B\_HEME; UNKNOWN\_1.  
 DR PROSITE; PS00022; EGF\_1; 10.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS01248; LAMININ\_TYPE\_EGF; 12.  
 DR PROSITE; PS00119; PA2\_ASP; UNKNOWN\_1.  
 KW Laminin EGF-like domain.  
 SQ SEQUENCE 1799 AA; 196577 MW; 37CA24B9CDA0791F CRC64;

Query Match 29.4%; Score 60; DB 2; Length 1799;  
 Best Local Similarity 29.8%; Pred. No. 1e+02;  
 Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

OY 5 YQKCHCHM-----GTHCHSSD-GPRGVPEPRC 32  
 Db 1111 FTGQCHCHAGGRTCEQELVWGDPLQCRACDCDPRG-IDKPOC 1156

RESULT 13  
 LMB2\_RAT  
 ID LMB2\_RAT  
 AC P15800;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Laminin beta-2 chain precursor (S-laminin) (Laminin chain B3).  
 GN Name=Lamb2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=89159410; PubMed=2922051;  
 RA Hunter D.D., Shah V., Merlie J.P., Sanes J.R.;  
 RA "A laminin-like adhesive protein concentrated in the synaptic cleft of  
 RT the neuromuscular junction.";  
 RL Nature 338:229-234(1989).  
 CC -!- FUNCTION: Binding to cells via a high affinity receptor, laminin  
 CC is thought to mediate the attachment, migration and organization  
 CC of cells into tissues during embryonic development by interacting  
 CC with other extracellular matrix components.  
 CC -!- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
 CC different polypeptide chains (alpha, beta, gamma), which are bound  
 CC to each other by disulfide bonds into a cross-shaped molecule

FT	DISULFID	473	487	By similarity.
FT	DISULFID	475	494	By similarity.
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FT	DISULFID	496	504	By similarity.
FT	DISULFID	508	522	By similarity.
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FT	DISULFID	819	831	By similarity.
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FT	DISULFID	991	1010	By similarity.
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FT	DISULFID	1025	1038	By similarity.
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FT	DISULFID	1100	1117	By similarity.
FT	DISULFID	1119	1128	By similarity.
FT	DISULFID	1131	1143	By similarity.
FT	DISULFID	1146	1158	By similarity.
FT	DISULFID	1148	1165	By similarity.
FT	DISULFID	1157	1176	By similarity.
FT	DISULFID	1179	1190	By similarity.
FT	DISULFID	1193	1193	Interchain (Probable).
FT	DISULFID	1196	1196	Interchain (Probable).
FT	DISULFID	1800	1800	Interchain (Probable).
FT	CARBOHYD	251	251	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	371	371	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1088	1088	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1252	1252	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1311	1311	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1351	1351	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1502	1502	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	1502	1502	N-linked (GlcNAc. .) (Potential).
FT	SEQUENCE	1801 AA; 196473 MW; 97AEF32F8F31FA75 CRC64;		
Query Match		29.4%; Score 60; DB 1; Length 1801;		
Best Local Similarity		29.8%; Pred. No. 1e+02;		
Matches 14; Conservative		5; Mismatches 8; Indels 20; Gaps 3;		
QY	5 YGKCHCHCHM-----GTHCHSSD-GPRGVPEPRC 32			
Db	1113 FTGQCHCHAGFGRTCTCEQELHWGDPGLQCRACDCDPRG-IDKPOC 1158			
RESULT 14				
YHL1_EBV				
ID_YHL1_EBV	STANDARD; PRT; 560 AA.			
AC				
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	29-MAR-2004 (Rel. 43, Last annotation update)			
DE	Hypothetical BHLFI protein.			
OS	Epstein-Barr virus (strain B95-8) (HHV-4) (Human herpesvirus 4).			
OC	Viruses; dsDNA viruses, no RNA stage; Herpesviridae;			
OC	Gammaparvovirinae; Lymphocryptovirus.			
OX	NCBI_TaxId=10377;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84270667; PubMed=6087149;			
RA	Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,			
RA	Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,			
RA	Tufnell P.S., Barrett B.G.;			
RL	"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";			
RL	Nature 310:207-211(1984).			



```

RT Epstein-Barr virus."
RL EMBL J. 3:1083-1090(1984).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84222045; PubMed=6328526;
RA Yates J., Warren N., Reisman D., Sugden B.;
RT "A cis-acting element from the Epstein-Barr viral genome that permits
RT stable replication of recombinant plasmids in latently infected
RT cells."
RL Proc. Natl. Acad. Sci. U.S.A. 81:3806-3810(1984).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=84247360; PubMed=6330697;
RA Gibson T., Stockwell P., Ginsburg M., Barrell B.;
RT "Homology between two EBV early genes and HSV ribonucleotide reductase
RT and 38K genes."
RL Nucleic Acids Res. 12:5087-5099(1984).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=87289053; PubMed=3039467;
RA Bodescot M., Perricaudet M.;
RT "Clustered alternative splice sites in Epstein-Barr virus RNAs."
RL Nucleic Acids Res. 15:5887-5887(1987).
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RX MEDLINE=91021036; PubMed=2171209;
RA Parker B.D., Bankier A., Satchwell S., Barrell B., Farrell P.J.;
RT "Sequence and transcription of Raji Epstein-Barr virus DNA spanning
RT the B95-8 deletion region."
RL Virology 179:339-346(1990).
RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RA Hatfull G.F., Barrell B.G., Quinn J., McGeoch D.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=B95-8;
RA Binne U.K., Amon W., Farrell P.J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ507799; CAD53473.1;
SQ SEQUENCE 660 AA; 66244 MW; 86DA1D67A37152A2 CRC64;

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Query Match      29.2%; Score 59.5; DB 2; Length 660;
Best Local Similarity 57.1%; Pred. No. 45;
Matches 12; Conservative 1; Mismatches 7; Indels 1; Gaps 1;

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QY      13 MGTHCHSSDGRGVIPRCP 33
Db      1 MGTPCQARGPR-TTLPHP 20

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Search completed: November 16, 2004, 19:14:36  
Job time : 40.0515 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 35.1008 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHGTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	33	4 AAE02773	Aae02773 Human Nkp
2	204	100.0	33	8 ADQ30926	Adq30926 Human Nkp
3	204	100.0	190	2 AAY06401	Aay06401 Human B-C
4	204	100.0	190	4 AAE02769	Aae02769 Human Nkp
5	204	100.0	190	8 ADO19810	Ado19810 Human PRO
6	204	100.0	190	8 ADQ30923	Adq30923 Human Nkp
7	61.5	30.1	82	3 AAG35071	Aag35071 Arabidops
8	61.5	30.1	82	3 AAG11882	Aag11882 Arabidops
9	61.5	30.1	636	4 AAB66269	Aab66269 Rat TANGO
10	60	29.4	66	4 AAO10665	Aao10665 Human pol
11	60	29.4	201	2 AAY06403	Aay06403 Human B-C
12	60	29.4	1799	5 AAM50359	Aam50359 Mouse lam
13	60	29.4	1801	2 AAW50895	Aaw50895 Rat lamin
14	60	29.4	1801	7 ADE60383	Ade60383 Rat Prote
15	59	28.9	57	4 AAU43863	Aau43863 Propionib
16	59	28.9	57	6 ABM40382	Abm40382 Propionib
17	59	28.9	2813	2 AAW54347	Aaw54347 Canine vo
18	59	28.9	2813	3 AAY70557	Aay70557 Canine vo
19	58.5	28.7	77	5 ABB97268	Abb97268 Novel hum
20	58.5	28.7	148	2 AAY74028	Aay74028 Human pro
21	58.5	28.7	148	4 AAG74543	Aag74543 Human col
22	58.5	28.7	302	4 AEG03692	Aeg03692 Novel hum
23	58.5	28.7	2469	5 AAE18207	Aae18207 Human MOL
24	58.5	28.7	2469	7 ADD18192	Add18192 Human mol
25	58.5	28.7	2471	2 AAO27065	Aao27065 Human Not

#### ALIGNMENTS

RESULT 1

AAE02773

ID AAE02773 standard; peptide; 33 AA.

XX

AC AAE02773;

XX

DT 06-AUG-2001 (first entry)

XX

DE Human Nkp30 receptor intracellular region sequence.

XX

KW Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
therapy; intracellular region.

XX

OS Homo sapiens.

XX

PN WO200136630-A2.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-EP011697.

XX

PR 15-NOV-1999; 99CA-02288307.

XX

PA 15-NOV-1999; 99US-00440514.

XX

PA (INNA-) INNATE PHARMA SAS.

XX

PI (UYGE-) UNIV GENOVA.

XX

PI Moretta A, Bottino C, Biassoni R;

XX

WPI; 2001-329221/34.

XX

Novel compound, useful for detection and/or quantifying the presence of NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX

PS Claim 1; Fig 7B; 83pp; English.

XX

The invention relates to human Nkp30 receptor and its corresponding cDNA molecule which is involved in natural cytotoxicity mediated by natural killer (NK) cells and antibodies that identify the same. Nkp30 receptor is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively expressed on the surface of human mature NK cells. Nkp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide kits for detecting and/or quantifying the presence of NK cells, for the selective removal of NK cells from a biological sample, for the positive and selective purification of NK cells from a biological sample and for the in vitro

Query Match 100.0%; Score 204; DB 8; Length 33;

Qy 1 STVYQKCHCMGTHCHSSDGRGVIPEPRCP 33  
|||||

Db 1 STVYQKCHCMGTHCHSSDGRGVIPEPRCP 33  
|||||

Query Match: 100.0%; Score 204; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.2e-17;

ID AA106401 standard; protein; 190 aa.  
XX  
AC AAY06401;

Human B-cell myelin oligodendrocyte glycoprotein BMOG.

MBOG; B-cell myelin oligodendrocyte glycoprotein; human; signal transduction; immunomodulator; antiinflammatory; autoimmune disease; inflammation; gene therapy diagnosis.

OS Homo sapiens.

xx	FH	Key	Location/Qualifiers

```
FT peptide
1.12 /note= "leader peptide"
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FT  
F10000  
13. 1.130  
/note= "mature protein"

PT	Modified base	note= "N-glycosylated"
12		

FT	modified-price	00	/note= "N-glycosylated"
----	----------------	----	-------------------------

FI	Modelled-size	121	
FT		/note= "N-glycosylated"	

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FT DOMAIN
133: .162
/note= "transmembrane d

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FT	REPTIDE	166..190	/note= "alternatively spliced
FT			

XX PN WO9923867-A2.

20-MAY-1999.

05-NOV-1998;

XX  
PR 07-NOV-1997: 97US-0064761P.

PA (BIOU ) BIOGEN INC.  
XX

FI BROWLING O;  
XX  
DR WPI; 1999-418423/35.  
DR N-PSDB; AAX59347.  
XX  
PT Novel B-cell mvein oligodendrocyte glycoproteins

Claim 2, Page 42; 43pp; English.





XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for  
PT treating an immune related disorder such as systemic lupus erythematosus,  
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or  
PT spondyloarthritis.  
XX  
XX Claim 7; SEQ ID NO 734; 1731pp; English.

XX The invention relates to human PRO polypeptides and the polynucleotides  
CC encoding them. The polypeptides and polynucleotides are useful for  
CC treating and diagnosing immune related disorders in mammals. The immune  
CC related disorders include systemic lupus erythematosus, rheumatoid  
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
CC central or peripheral nervous system, demyelinating polyneuropathy,  
CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
CC invention.

XX SQ Sequence 190 AA;

Query Match 100.0%; Score 204; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 33  
D5 158 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 190

RESULT 6  
ADQ30923  
ID ADQ30923 standard; protein; 190 AA.

XX AC ADQ30923;  
XX  
XX 23-SEP-2004 (first entry)  
XX Human NKp30 polypeptide.  
XX Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Region 19..138  
XX /label= Extracellular region  
XX /note= "Region specifically described in Claim 3"  
XX Region 20..133  
XX /label  
XX /note= "Immunogenic peptide specifically described in  
XX Claim 3"  
XX Region 139..157  
XX /label= Transmembrane region  
XX /note= "Region specifically described in Claim 3"  
XX Region 158..190  
XX /label= Cytoplasmic tail  
XX /note= "Region specifically described in Claim 3"  
XX  
XX WO2004056392-A1.  
XX  
XX 08-JUL-2004.  
XX  
XX 22-DEC-2003; 2003WO-EP014716.  
XX  
XX 23-DEC-2002; 2002US-0435344P.  
XX  
XX (INNA-) INNATE PHARMA.  
XX  
XX Romagne F, Andre P;  
XX

DR WPI; 2004-507595/48.  
XX  
XX Pharmaceutical compositions that stimulate proliferation of natural  
PT killer cells useful for therapy of melanoma, chronic myeloid, and  
PT leukemia, comprise an anti-natural killer cell receptor antibody and  
PT interleukins.  
XX  
XX Claim 3; SEQ ID NO 1; 35pp; English.

XX The present sequence is that of human NKp30, a 190 amino acid polypeptide  
CC (about 30 kDa on SDS-PAGE) that is selectively expressed by natural  
CC killer (NK) cells, and particularly by mature NK cells. Claimed  
CC pharmaceutical compositions that have a stimulating effect on the  
CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
CC antibody(ies) and cytokine(s) being administered together or separately  
CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
CC antigen-binding fragment which specifically binds to NKp30 or to a  
CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,  
CC when used for daily subcutaneous injection, comprising from 1 ng to 100  
CC mg/kg (body weight) of antibody(ies), and lower than 1 million  
CC units/square meters/day of cytokine(s), are useful for the prevention,  
CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute  
CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung  
CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,  
CC palliation and therapy (claimed).

XX SQ Sequence 190 AA;

Query Match 100.0%; Score 204; DB 8; Length 190;  
Best Local Similarity 100.0%; Pred. No. 6.9e-17;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 33  
D5 158 STVYQKCHCHMGTHCHSSDGRGVPEPRCP 190

RESULT 7  
AAG35071  
ID AAG35071 standard; protein; 82 AA.

XX AC AAG35071;  
XX  
XX 18-OCT-2000 (first entry)  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 42786.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
XX  
XX EP1033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
XX  
XX 25-FEB-1999; 99US-0121825P.  
XX 09-MAR-1999; 99US-0123180P.  
XX 23-MAR-1999; 99US-0123548P.  
XX 25-MAR-1999; 99US-0125788P.  
XX 29-MAR-1999; 99US-0126264P.  
XX 01-APR-1999; 99US-0126785P.  
XX 06-APR-1999; 99US-0127462P.  
XX 08-APR-1999; 99US-0128234P.  
XX 16-APR-1999; 99US-0129845P.  
XX 19-APR-1999; 99US-0130077P.  
XX 21-APR-1999; 99US-0130449P.



us-10-036-444-6.open.rag

Wed Nov 17 05:46:43 2004

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PR 14-OCT-1999; 99US-0159637P.
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PR 25-OCT-1999; 99US-0161404P.
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PR 26-OCT-1999; 99US-0161360P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
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PR 28-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 61.5; DB 3; Length 82;
Best Local Similarity 52.4%; Pred. No. 6.5;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VYQKCHCHMGTHCHSSDCP 23
Db 48 LFSDEKCH-HLKLHCGSSHP 67

RESULT 8
AAG11882
ID AAG11882 standard; protein; 82 AA.
XX AC AAG11882;
XX XX
XX 17-OCT-2000 (first entry)
XX XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 10773.
XX DE
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX OS
XX Arabidopsis thaliana.
XX PN
XX EP1033405-A2.
XX PD
XX 06-SEP-2000.
XX XX
XX 25-FEB-2000; 2000EP-00301439.
XX XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
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XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.
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PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159223P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 14-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 18-OCT-1999; 99US-0159638P.  
PR 21-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.

PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 30.1%; Score 61.5; DB 3; Length 82;

Best Local Similarity 52.4%; Pred. No. 6.5;

Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 3 VYVQKCHCHMGTHCHSSDGP 23

DB 48 LFSDGKCH-HLKLHCGSSHGP 67

RESULT 9

AAB66269

ID AAB66269 standard; protein; 636 AA.

XX AC AAB66269;

XX DT 05-APR-2001 (first entry)

XX DE Rat TANGO 272 SEQ ID NO: 20.

XX KW Membrane associated protein; secreted protein; human; mouse; rat;

XX KW INTERCEPT 340; MANGO 003; MANGO 347; TANGO 272; TANGO 295; TANGO 354;

XX KW TANGO 378; skeletal disorder; cardiovascular disorder; renal disorder;

XX KW haematopoietic disorder; neural disorder; hepatic disorder;

XX OS Rattus sp.

XX PN WO200100673-A1.

XX PD 04-JAN-2001.

XX PF 29-JUN-2000; 2000WO-US018198.

XX PR 30-JUN-1999; 99US-00345464.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Barnes TM, Fraser CC, Wrighton N, Myers P, Busfield SJ, Sharp JD;

XX DR WPI; 2001-050128/06.

XX DR N-PSDB; AAP27791.

XX PT Isolated secreted or transmembrane proteins are used for diagnosis and

XX PT treatment of neoplastic and hematopoietic disorders e.g. T cell

XX PS Claim 9; Page 238-240; 294pp; English.

XX CC The present invention provides the protein and coding sequences for a

XX CC number of membrane associated and secreted proteins from human, mouse and

XX CC rat. The proteins are designated INTERCEPT 340, MANGO 003, MANGO 347,

XX CC TANGO 272, TANGO 295, TANGO 254 and TANGO 378. The proteins are all

XX CC involved in signal transduction and the sequences can be used in the

XX CC treatment of cardiovascular, renal, hepatic, neural, neoplastic, skeletal

XX CC and haematopoietic disorders

XX SQ Sequence 636 AA;

Query Match 30.1%; Score 61.5; DB 4; Length 636;  
Best Local Similarity 44.4%; Pred. No. 49;  
Matches 12; Conservative 0; Mismatches 12; Indels 3; Gaps 1;  
Qy 9 CHCHGTHCHSSDGRGVIP---EPRC 32  
Db 411 CQCHGATCPDQSGSCVCIPGTGPNC 437

RESULT 10  
AAO10665  
ID AAO10665 standard; protein; 66 AA.  
XX AAO10665;  
AC AAO10665;  
XX 06-NOV-2001 (first entry)  
XX Human polypeptide SEQ ID NO 24557.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
XX tissue growth factor; immunomodulatory; cancer; leukaemia;  
XX nervous system disorders; arthritis; inflammation.  
XX Homo sapiens.  
XX WO200164835-A2.  
XX 07-SEP-2001.  
XX 26-FEB-2001; 2001WO-US004927.  
XX 28-FEB-2000; 2000US-00515126.  
XX 18-MAY-2000; 2000US-00577409.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-514838/56.  
XX N-PSDB; AA190596.

Isolated nucleic acids and polypeptides, useful for preventing diagnosing  
and treating e.g. leukemia, inflammation and immune disorders.  
XX Claim 20; SEQ ID NO 24557; 1399pp + Sequence Listing; English.  
XX The invention relates to human polynucleotides (AA179941-AA193841) and  
XX the encoded proteins (AAO00010-AAO1910) that exhibit activity relating to  
XX cytokine, cell proliferation or cell differentiation or which may induce  
XX production of other cytokines in other cell populations. The  
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or  
XX peptide therapy. The polypeptides have various cytokine-like activities,  
XX e.g. stem cell growth factor activity, haematopoiesis regulating  
XX activity, tissue growth factor activity, immunomodulatory activity and  
XX activin/inhibin activity, and may be useful in the diagnosis and/or  
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and  
XX inflammation. Note: The sequence data for this patent did not form part  
XX of the printed specification, but was obtained in electronic format  
XX directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX Sequence 66 AA;

Query Match 29.4%; Score 60; DB 4; Length 66;  
Best Local Similarity 37.0%; Pred. No. 7.9;  
Matches 10; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 4 YQCKCHCHGTHCHSSDGRGVIP 30  
Db 27 HHHHCHCHVHSHHNSQHPPPPPP 53

RESULT 11  
AAO06403  
ID AAY06403 standard; protein; 201 AA.  
XX AAY06403;  
AC AAY06403;  
XX 20-SEP-1999 (first entry)  
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
XX signal transduction; immunomodulator; antiinflammatory;  
XX autoimmune disease; inflammation; gene therapy; diagnosis.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..12  
FT Protein /note= "leader peptide"  
FT Protein 13..201  
FT Modified-site 42 /note= "mature protein"  
FT Modified-site 68 /note= "N-glycosylated"  
FT Modified-site 121 /note= "N-glycosylated"  
FT Domain 139..162 /note= "N-glycosylated"  
FT Peptide /note= "transmembrane domain"  
FT Peptide 166..201 /note= "alternatively spliced C-terminal end"  
XX WO9923867-A2.  
XX 20-MAY-1999.  
XX 05-NOV-1998; 98WO-US023826.  
XX 07-NOV-1997; 97US-0064761P.  
XX (BIOI) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59349.  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX Claim 2; Page 43; 43pp; English.  
XX This sequence represents human BMOG, a novel member of the B cell myelin  
XX oligodendrocyte glycoprotein family that is expressed by germinal centre  
XX B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were  
XX identified. The protein is present primarily in the spleen, in lymph  
XX nodes and in germinal centre B cells. It may have immunoregulatory  
XX functions, and soluble or chimeric fusion proteins of BMOG may be used to  
XX regulate the immune system in autoimmune or inflammatory disease. Vectors  
XX comprising BMOG, prokaryotic and eukaryotic host cells, and a method of  
XX producing BMOG using these transformed host cells are also provided. BMOG  
XX polypeptides can be used for modulating the immune system of a subject or  
XX to inhibit signal transduction in a cell expressing BMOG by contacting it  
XX with a soluble BMOG protein. The nucleic acid can be used for gene  
XX therapy. The protein can also be used to target a toxin, imaging agent or  
XX radionuclide to a cell expressing BMOG. (All claimed)  
XX Sequence 201 AA;

Query Match 29.4%; Score 60; DB 2; Length 201;  
Best Local Similarity 43.2%; Pred. No. 24;  
Matches 16; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

Qy 1 STVYQKCHCHGTHCHSSDGRP----GVIPRCP 33

Db 158 STVYQK-----CLTWGRRQLPAVVAPLPP 186  
 ||||| | : ||| | : | | |

RESULT 12  
 AAW50359  
 ID AAW50359 standard; protein; 1799 AA.  
 XX  
 AC AAW50359;  
 XX  
 DT 18-FEB-2002 (first entry)  
 XX  
 DE Mouse laminin-15 beta 2 chain.

XX  
 KW Laminin-15; mouse; retina; eye; therapy; ophthalmological;  
 KW antiinflammatory; rod dystrophy; rod-cone dystrophy;  
 KW retinitis pigmentosa; macular degeneration; retinal detachment.  
 XX  
 OS Mus musculus.  
 XX WO200183516-A1.  
 XX  
 XX 08-NOV-2001.

XX 01-MAY-2001; 2001WO-US013943.

XX 01-MAY-2000; 2000US-0200863P.

XX (MASS-) MASSACHUSETTS GEN HOSPITAL.

XX Burgeson RE, Brunken W, Champlaud M, Hunter D;  
 XX WPI; 2002-041478/05.

XX Novel substantially pure preparation comprising laminin having laminin  
 PT chain alpha 5, beta 2, and gamma 3, useful for treating retinal disorders  
 PT such as retinitis pigmentosa, macular degeneration, retinal detachment.  
 XX  
 PS Disclosure; Fig 3A; 58pp; English.

XX The present sequence is that of the beta 2 chain of mouse laminin-15, a  
 CC novel member of the laminin family that is produced in the retina. The  
 CC retina produces 2 novel laminin trimers; laminin-14 (alpha 4, beta 2,  
 CC gamma 3) and laminin-15 (alpha 5, beta 2, gamma 3). These are expressed  
 CC within the inter-photoreceptor matrix and in the outer plexiform layer,  
 CC and may serve to stabilise retinal synapses. The invention provides  
 CC laminin-15 preparations and cells comprising a nucleic acid encoding the  
 CC laminin alpha 5, beta 2 and gamma 3 chains, and which are capable of  
 CC producing laminin-15. The laminin-15 preparation is used in claimed  
 CC methods of: increasing retina immunophotoreceptor matrix stability;  
 CC increasing the stability of retina photoreceptor compounds, especially an  
 CC outer segment, inner segment or synapse; increasing retina adhesion;  
 CC treating a disorder associated with retina degeneration, especially rod  
 CC dystrophy, rod-cone dystrophy, retinitis pigmentosa, macular degeneration  
 CC and retinal detachment; increasing the stability of synapses of the  
 CC central nervous system or peripheral nervous system; stimulating  
 CC neuroregeneration, axon outgrowth or synapse formation; preparing an  
 CC implant, e.g. a catheter, artificial joint, retinal implant, timed  
 CC releasing device, neural cell growth guide or artificial tissue, by  
 CC coating with the laminin-15 preparation; and increasing photosensitivity  
 CC by implanting a tip coated with the laminin-15 preparation into an eye.  
 CC The laminin may be recombinant, and the 3 chains co-expressed in the same  
 CC cell or expressed in different cells

XX SQ Sequence 1799 AA;

Query Match 25.4%; Score 60; DB 5; Length 1799;  
 Best Local Similarity 25.8%; Pred. No. 2.1e+02;  
 Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGRCHM-----GTHCHSD-GPRGVIEPRC 32

Db 1111 FTGQCHAGRGRCBCELYWGDPLQCRACDCDPRG-IDKPOC 1156

RESULT 13  
 AAW50895  
 ID AAW50895 standard; protein; 1801 AA.  
 XX  
 AC AAW50895;  
 XX  
 DT 07-DEC-1998 (first entry)  
 XX  
 DE Rat laminin B2 chain.

XX  
 KW Laminin; rat; beta-amyloid; amyloidosis; Alzheimer's disease;  
 KW Down's syndrome; hereditary cerebral haemorrhage; inflammation;  
 KW malignancy; Familial Mediterranean Fever; multiple myeloma;  
 KW type II diabetes; prion disease; Creutzfeldt-Jacob disease; CJD;  
 KW Gerstmann-Strausler disease; Creutzfeldt-Jacob disease; CJD;  
 KW carpal tunnel syndrome; senile cardiac amyloid polynuropathy;  
 KW Familial Amyloidotic Polynuropathy; thyroid carcinoma; diagnosis;  
 KW therapy.

XX Rattus sp.

XX WO9815179-A1.

XX 16-APR-1998.

XX 08-OCT-1997; 97WO-US018145.

XX 08-OCT-1996; 96US-0027981P.

XX (UNIV ) UNIV WASHINGTON.

XX Castillo G, Snow AD;  
 XX WPI; 1998-240534/21.

XX Use of laminin and fragments - for developing products for use in the  
 PT diagnosis and treatment of amyloid disease, e.g. Alzheimer's disease or  
 PT CJD.  
 XX  
 XX Claim 15; Page 94-97; 132pp; English.  
 XX  
 XX This is the amino acid sequence of the rat laminin B2 chain. The primary  
 CC object of the invention is to use laminin, laminin-derived protein  
 CC fragments and/or laminin-derived polypeptides as potent inhibitors of  
 CC amyloid formation, deposition, accumulation and/or persistence in  
 CC Alzheimer's disease and other amyloidoses. The laminin products (see  
 CC AAW50888-98) may include mammalian laminin A or A1 chain, laminin B1 or  
 CC B2 chain, laminin A2 chain (merosin), laminin G1 chain, the globular  
 CC repeats of the laminin A1 chain and the beta-amyloid binding domain of  
 CC the laminin A chain. A claimed method for treating an amyloid disease  
 CC comprises administering a polypeptide having a conformational similarity  
 CC to a fragment of a laminin protein. A method for diagnosing an amyloid  
 CC disease involves determining levels of laminin in a sample. Production of  
 CC laminin or its fourth globular repeat in vivo provides a method for in  
 CC vivo inhibition of beta-amyloid amyloidosis. The products and methods can  
 CC be used for the diagnosis, prognosis, monitoring and treatment of  
 CC amyloidoses such as Alzheimer's disease, Down's syndrome and hereditary  
 CC cerebral haemorrhage with amyloidosis of the Dutch type (where the  
 CC specific amyloid is the beta-amyloid protein), the amyloidosis associated  
 CC with chronic inflammation, various forms of malignancy and familial  
 CC Mediterranean Fever (AA amyloid or inflammation-association amyloidosis),  
 CC the amyloidosis associated with multiple myeloma and other B-cell  
 CC abnormalities (AL amyloid), the amyloidosis associated with type II  
 CC diabetes (amylin or islet amyloid), the amyloidosis associated with prion  
 CC diseases including Creutzfeldt-Jacob disease, Gerstmann-Strausler  
 CC syndrome, Kuru and animal scrapie (P+P amyloid), the amyloidosis  
 CC associated with long-term haemodialysis and carpal tunnel syndrome (beta  
 CC 2-microglobulin amyloid), the amyloidosis associated with senile cardiac  
 CC amyloid and Familial Amyloidotic Polynuropathy (prealbumin or  
 CC transthyretin amyloid), and the amyloidosis associated with endocrine  
 CC tumours such as medullary carcinoma of the thyroid (variant of

CC procalcitonin)

XX SQ Sequence 1801 AA;

Query Match 29.4%; Score 60; DB 2; Length 1801;

Best Local Similarity 29.8%; Pred. No. 2.1e+02;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVIPPRC 32

Db 1113 FTGQCHCHAGGRTCTCQELHWGDPGLQCRACDCPRG-IDKPOC 1158

RESULT 14

AD60383

AC ADE60383 standard; protein; 1801 AA.

XX AC ADE60383;

XX AC ADE60383;

DT 29-JAN-2004 (first entry)

DE Rat Protein P15800, SEQ ID NO 6292.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P15800.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC the sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1801 AA;

Query Match 29.4%; Score 60; DB 7; Length 1801;

Best Local Similarity 29.8%; Pred. No. 2.1e+02;

Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQGKCHCHM-----GTHCHSSD-GPRGVIPPRC 32

Db 1113 FTGQCHCHAGGRTCTCQELHWGDPGLQCRACDCPRG-IDKPOC 1158

RESULT 15

AAU43863

ID AAU43863 standard; protein; 57 AA.

XX AC AAU43863;

XX AC AAU43863;

DT 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #4759.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US012865.

XX 21-APR-2000; 2000US-0199047P.

PR 02-JUN-2000; 2000US-0208841P.

PR 07-JUL-2000; 2000US-0216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

DR N-PSDB; AAS59521.

XX Propionibacterium acnes polypeptides and nucleic acids useful for

PT vaccinating against and diagnosing infections, especially useful for

PT treating acne vulgaris.

XX Example 1; SEQ ID NO 5058; 1069pp; English.

XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis) uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as



CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for  
CC this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

xx

SQ Sequence 57 AA;

Query Match 28.9%; Score 59; DB 4; Length 57;  
Best Local Similarity 40.0%; Pred. No. 9.1; Indels 0; Gaps 0;  
Matches 10; Conservative 4; Mismatches 11;

QY 9 CHCHMGTHCHSSDGRGVPEPRCP 33

Db 3 CHGNLGTGPHADTGTGVSQPSRP 27

Search completed: November 16, 2004, 18:56:01  
Job time : 38.1008 secs

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# OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 29.4987 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204  
Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	33	US-10-036-444-6	Sequence 6, Appli
2	204	100.0	190	US-10-036-444-2	Sequence 2, Appli
3	204	100.0	190	US-10-036-259-4	Sequence 4, Appli
4	169.5	83.1	185	US-10-036-259-7	Sequence 7, Appli
5	62	30.4	145	US-10-437-963-200771	Sequence 200771,
6	61.5	30.1	636	US-09-796-753-100	Sequence 100, App
7	61.5	30.1	636	US-09-796-753-124	Sequence 124, App
8	61	29.9	201	US-10-425-115-264880	Sequence 264880,
9	60	29.4	201	US-10-036-259-6	Sequence 6, Appli
10	60	29.4	1799	US-03-845-583-6	Sequence 6, Appli
11	60	29.4	1801	US-03-938-275-8	Sequence 8, Appli
12	59	28.9	160	US-10-424-599-166699	Sequence 166699,
13	59	28.9	2813	US-09-886-900-2	Sequence 2, Appli

14	58.5	28.7	148	14	US-10-106-698-5317	Sequence 5317, Ap
15	58.5	28.7	1015	15	US-10-419-026-1	Sequence 1, Appli
16	58.5	28.7	2203	16	US-10-322-281-726	Sequence 726, App
17	58.5	28.7	2469	17	US-10-190-115-2	Sequence 2, Appli
18	58.5	28.7	2469	15	US-10-369-072-2	Sequence 2, Appli
19	58.5	28.7	2471	17	US-10-720-896A-12	Sequence 12, Appli
20	58	28.4	845	9	US-09-983-531A-6	Sequence 6, Appli
21	57.5	28.2	89	15	US-10-424-599-190841	Sequence 190841,
22	56.5	27.7	969	15	US-10-052-648A-34	Sequence 34, Appli
23	56.5	27.7	969	15	US-10-052-648A-35	Sequence 35, Appli
24	56	27.5	100	17	US-10-425-115-334473	Sequence 115759,
25	56	27.5	135	16	US-10-437-963-115759	Sequence 36099, A
26	56	27.5	239	16	US-10-767-701-36099	Sequence 272280,
27	55.5	27.2	125	15	US-10-424-599-272280	Sequence 358052,
28	55.5	27.2	128	17	US-10-425-115-358052	Sequence 9, Appli
29	55.5	27.2	198	16	US-10-026-259-9	Sequence 20, Appli
30	55.5	27.2	601	9	US-09-802-582-20	Sequence 20, Appli
31	55.5	27.2	601	14	US-10-365-227-20	Sequence 2, Appli
32	55.5	27.2	1140	14	US-10-092-390-2	Sequence 33, Appli
33	55.5	27.2	1140	15	US-10-052-648A-33	Sequence 1838, Ap
34	55.5	27.2	1140	16	US-10-408-765A-1838	Sequence 149149,
35	55	27.0	71	16	US-10-437-963-149149	Sequence 3183, Ap
36	54.5	26.7	580	14	US-10-128-714-3183	Sequence 8183, Ap
37	54.5	26.7	680	14	US-10-128-714-8183	Sequence 14, Appli
38	54.5	26.7	1535	14	US-10-189-971-14	Sequence 12, Appli
39	54.5	26.7	1570	14	US-10-189-971-12	Sequence 4, Appli
40	54.5	26.7	1593	14	US-10-189-971-4	Sequence 2, Appli
41	54.5	26.7	1628	14	US-10-189-971-2	Sequence 12, Appli
42	54.5	26.7	2710	13	US-10-153-273-12	Sequence 116, App
43	54	26.5	497	10	US-09-796-753-116	Sequence 302949,
44	54	26.5	698	17	US-10-425-115-302949	Sequence 4, Appli
45	54	26.5	928	15	US-10-052-648A-4	

## ALIGNMENTS

### RESULT 1

US-10-036-444-6  
; Sequence 6, Application US/10036444  
; Publication No: US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT APPLICATION NUMBER: US/10/036,444  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Human NK cell  
US-10-036-444-6

Query Match 100.0%; Score 204; DB 13; Length 33;

Best Local Similarity 100.0%; Pred. No. 9.4e-17; Mismatches 0; Indels 0; Gaps 0;

Matches 33; Conservative 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

Db 1 STVYQKCHCHMGTHCHSSDGRGVIPRCP 33

### RESULT 2

US-10-036-444-2

```

; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1e1 triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      100.0%; Score 204; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33
Db 158 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 190

RESULT 3
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/550,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match      100.0%; Score 204; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.8e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33
Db 158 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 190

RESULT 4
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/550,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match      83.1%; Score 169.5; DB 16; Length 185;
Best Local Similarity 87.9%; Pred. No. 5e-12;
Matches 29; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 STVYQKCHCHMGTHCHSSDGRGVIPEPRCP 33
Db 156 STVYHGKCHCHMGTHCHSSD---GVIPERCP 185

RESULT 5
US-10-437-963-200771
; Sequence 200771, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 200771
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96208C.1.pep
US-10-437-963-200771

Query Match      30.4%; Score 62; DB 16; Length 145;
Best Local Similarity 34.9%; Pred. No. 14;
Matches 15; Conservative 3; Mismatches 3; Indels 22; Gaps 3;

QY 12 HMGTHCHSSDGRGVI---PEP-----RCP 33
Db 36 HLAHCH-SDGPPGLACQPEPLPFVMSGVWTRARRSVRCP 77

RESULT 6
US-09-796-753-100
; Sequence 100, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.

```

```

/ / TITLE OF INVENTION:  SECRETED PROTEINS AND USES THEREOF
/ / FILE REFERENCE:  7853-227-999
/ / CURRENT APPLICATION NUMBER:  US/09/796,753
/ / CURRENT FILING DATE:  2001-03-01
/ / PRIOR APPLICATION NUMBER:  09/183,175
/ / PRIOR FILING DATE:  1998-10-30
/ / PRIOR APPLICATION NUMBER:  09/223,094
/ / PRIOR FILING DATE:  1998-12-30
/ / PRIOR APPLICATION NUMBER:  09/223,546
/ / PRIOR FILING DATE:  1998-12-30
/ / PRIOR APPLICATION NUMBER:  09/224,246
/ / PRIOR FILING DATE:  1998-12-30
/ / PRIOR APPLICATION NUMBER:  09/259,388
/ / PRIOR FILING DATE:  1999-02-26
/ / PRIOR APPLICATION NUMBER:  60/122,458
/ / PRIOR FILING DATE:  1999-03-01
/ / PRIOR APPLICATION NUMBER:  09/312,359
/ / PRIOR FILING DATE:  1999-05-14
/ / PRIOR APPLICATION NUMBER:  09/336,536
/ / PRIOR FILING DATE:  1999-06-18
/ / PRIOR APPLICATION NUMBER:  09/342,687
/ / PRIOR FILING DATE:  1999-06-29
/ / PRIOR APPLICATION NUMBER:  09/345,464
/ / PRIOR FILING DATE:  1999-06-30
/ / PRIOR APPLICATION NUMBER:  09/365,164
/ / PRIOR FILING DATE:  1999-07-30
/ / PRIOR APPLICATION NUMBER:  09/399,723
/ / PRIOR FILING DATE:  1999-09-20
/ / PRIOR APPLICATION NUMBER:  09/409,634
/ / PRIOR FILING DATE:  1999-09-30
/ / PRIOR APPLICATION NUMBER:  09/471,179
/ / PRIOR FILING DATE:  1999-12-23
/ / PRIOR APPLICATION NUMBER:  09/474,071
/ / PRIOR FILING DATE:  1999-12-29
/ / PRIOR APPLICATION NUMBER:  09/474,072
/ / PRIOR FILING DATE:  1999-12-29
/ / PRIOR APPLICATION NUMBER:  09/514,010
/ / PRIOR FILING DATE:  2000-02-25
/ / PRIOR APPLICATION NUMBER:  09/516,745
/ / PRIOR FILING DATE:  2000-03-01
/ / PRIOR APPLICATION NUMBER:  09/572,002
/ / PRIOR FILING DATE:  2000-05-14
/ / PRIOR APPLICATION NUMBER:  09/597,993
/ / PRIOR FILING DATE:  2000-06-19
/ / PRIOR APPLICATION NUMBER:  09/599,596
/ / PRIOR FILING DATE:  2000-06-22
/ / PRIOR APPLICATION NUMBER:  09/630,334
/ / PRIOR FILING DATE:  2000-07-31
/ / PRIOR APPLICATION NUMBER:  09/606,565
/ / PRIOR FILING DATE:  2000-06-29
/ / PRIOR APPLICATION NUMBER:  09/606,317
/ / PRIOR FILING DATE:  2000-06-29
/ / PRIOR APPLICATION NUMBER:  09/665,666
/ / PRIOR FILING DATE:  2000-09-20
/ / PRIOR APPLICATION NUMBER:  09/677,751
/ / PRIOR FILING DATE:  2000-09-30
/ / NUMBER OF SEQ ID NOS:  162
/ / SEQ ID NO 100
/ / LENGTH:  636
/ / TYPE:  PRT
/ / ORGANISM:  Rattus sp.
/ / IS-09-796-753-100

```

Query Match 30.1%; Score 61.5; DB 10; Length 636;  
Best Local Similarity 44.4%; Pred. No. 64;  
Matches 12: Conservative 0; Mismatches 12; Indels 3

Qy 9 CHCHMGTHCHSSDGPGRVIP---EPRC 32  
Db 411 CQCHHGATCHPQDGGSCVCIPTGWTGPNC 437

## RESULT 7

```

US-09-796-753-124
; Sequence 124, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 124
; LENGTH: 636
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-09-796-753-124

```

Query Match 30.1%; Score 61.5; DB 10; Length 636;  
Best Local Similarity 44.4%; Pred. No. 64;  
Matches 12: Conservative 0; Mismatches 12; Indels 3

9 CHCHMGTHCHSSDGPGRVIP--EPRC 32

Db  
411 CQCHHGATCHPQDGSVCIPGWTGPNC 437

## RESULT 8

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US-10-425-115-264880
; Sequence 264880, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhao, Yinhui
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 264880
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_173
US-10-425-115-264880

```

Query Match 29.9%; Score 61; DB 17; Length 201;  
Best Local Similarity 35.1%; Pred. No. 25;  
Matches 13; Conservative 5; Mismatches 9; Indels 10; Gaps 2;

**QY**    5 YQGKCHCMGTHCHSSDGPRIPE-----PRC 32  
         : : : : : : : : : : :  
**Dd**    26 FEARCTNKGHLHSHSGRGGRGV-PQAALVAGGGPRC 61

## RESULT 9

```

US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

```

Query Match 29.4%; Score 60; DB 16; Length 201;  
Best Local Similarity 43.2%; Pred. No. 33;  
Matches 16; Conservative 2; Mismatches 7; Indels 12; Gaps 2;

1 STVYQKCHCHMGTHCHSSDGR---GVIPERCP 33  
158 STVYQK-----CLTWKGRRLPAWVPALEPP 186  
Db

RESULT 10

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US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgesson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND US95 THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1759
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-6

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Query Match 29.4%; Score 60; DB 9; Length 1799;  
Best Local Similarity 29.8%; Pred. No. 2.5e+02;  
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

Qy 5 YQGKCHCM-----GTHCHSD-GPRGVIPRC 32  
          :|:||||               -      :|:|:|:|:  
Db 1111 FTGOCHCHAGFGGRCTSECQELYWGDPGLQCACDPRG-IDKPOC 1156

## RESULT, T 11

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US-09-938-275-8
RESOLU 11
; Sequence 8, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US2002011309Alvegius
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
US-09-938-275-8

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Query Match 29.4%; Score 60; DB 9; Length 1801;  
Best Local Similarity 29.8%; Pred. No. 2.5e+02;  
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

```

QY      5 YQGKCHCHM-----GTHCHSSD-GPRGVIPEPC 32
      : : : : :
      : : : : :
Db     1113 FTGQCHCHAGFGGRTSCQEQLHWGDPGLQCRACDCDPRG IDKPOC 1158

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DEPT. 12

US-10-424-598-166699  
 ; Sequence 166699, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yihua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Mo

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
;; FILE REFERENCE: 38-21(53223)B  
;; CURRENT APPLICATION NUMBER: US/10/424,599  
;; CURRENT FILING DATE: 2003-04-28  
;; NUMBER OF SEQ ID NOS: 285684  
;; SEQ ID NO 186699  
;; LENGTH: 160  
;; TYPE: PRT  
;; ORGANISM: Glycine max  
;; FEATURE:  
;; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_121544C.1.pap  
US-10-424-599-166699

Query Match 28.9%; Score 59; DB 15; Length 160;  
Best Local Similarity 50.0%; Pred. No. 34;  
Matches 12; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

QY 9 CHCHMG--THCHSSDGRGVIPER 30  
||| . . . . .  
DB 6 CHCSLGRAHCHYNH--RRVIPSP 27

RESULT 13  
US-09-886-900-2  
; Sequence 2, Application US/09886900  
; Patent No. US20020137051A1  
; GENERAL INFORMATION:  
; APPLICANT: Venta, Patrick J  
; Yuzbasiyan-Gurkan, Vilma  
; Schall, William D  
; Brewer, George J  
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND  
; FACTOR AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.B.C.  
; STREET: 5445 Corporate Drive  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48098  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/886,900  
; FILING DATE: 21-Jun-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/896,449  
; FILING DATE: 18-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, DeAnn F.  
; REFERENCE/DOCKET NUMBER: 2115-001226  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 248-641-1600  
; TELEFAX: 248-641-0270  
; TELEX: 287637  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2813 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-886-900-2  
Query Match 28.9%; Score 59; DB 9; Length 2813;  
Best Local Similarity 30.6%; Pred. No. 5e+02;  
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQKG-----CHCHMG-THCHSSDG-----PRGVIPERPC 32  
||| . . . . .  
DB 710 YYDGEIFQPEDIFSDHHTMCYCEDGFHCTTSGGLGSLLPNPVLSSPRC 758

RESULT 14  
US-10-106-698-5317  
; Sequence 5317, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 5317  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (18)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-5317

Query Match 28.7%; Score 58.5; DB 14; Length 148;  
Best Local Similarity 43.5%; Pred. No. 37;  
Matches 10; Conservative 2; Mismatches 8; Indels 3; Gaps 1;

QY 10 HCHMGTHCHSSDGRGVIPERPC 32  
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DB 83 HCHLGYRCHGRPQREGL---PRC 102

RESULT 15  
US-10-419-026-1  
; Sequence 1, Application US/10419026  
; Publication No. US20040058443A1  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, Spyridon  
; APPLICANT: Fortini, Mark  
; APPLICANT: Matsuno, Kenji  
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY DIFFERENTIATED CELLS USING THE  
; TITLE OF INVENTION: NOTCH PATHWAY  
; FILE REFERENCE: 10910-096  
; CURRENT APPLICATION NUMBER: US/10/419,026  
; CURRENT FILING DATE: 2003-04-18  
; PRIOR APPLICATION NUMBER: 08/537,210  
; PRIOR FILING DATE: 1995-09-29  
; PRIOR APPLICATION NUMBER: 09/113,824  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1015  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-419-026-1

Query Match 28.7%; Score 58.5; DB 15; Length 1015;  
Best Local Similarity 42.3%; Pred. No. 2.2e+02;  
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;

QY 7 GKCHCHMGTHC-HSSDGRGVIPERPC 31  
||| . . . . .

Wed Nov 17 05:46:44 2004

us-10-036-444-6.open.rapb

Page 6

Db 193 GQVKRKGEQCVHTASGPRCFCPSPR 218

Search completed: November 16, 2004, 19:45:07  
Job time : 31.4987 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 9.27851 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-6

Perfect score: 204

Sequence: 1 STVYQKCHCHMGTHCHSSDGRGVIPERCP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	29.4	1799	4 US-09-845-583A-6	Sequence 6, Appli
2	59	28.9	2813	3 US-08-896-449A-2	Sequence 2, Appli
3	59	28.9	2813	3 US-09-132-652-2	Sequence 2, Appli
4	59	28.9	2813	4 US-09-886-900A-2	Sequence 2, Appli
5	59	28.9	2813	4 US-09-662-478C-2	Sequence 2, Appli
6	58.5	28.7	1015	1 US-08-537-210A-1	Sequence 1, Appli
7	58.5	28.7	1015	3 US-09-113-825-1	Sequence 1, Appli
8	58.5	28.7	2471	1 US-08-185-432-16	Sequence 16, Appli
9	58.5	28.7	2471	1 US-08-083-590A-19	Sequence 19, Appli
10	58.5	28.7	2471	3 US-08-532-384-19	Sequence 19, Appli
11	58.5	28.7	2471	4 US-08-899-232-1	Sequence 1, Appli
12	58.5	28.7	2471	4 US-09-121-457-1	Sequence 1, Appli
13	57	27.9	92	4 US-09-270-767-38503	Sequence 38503, A
14	57	27.9	92	4 US-09-270-767-53720	Sequence 53720, A
15	54.5	26.7	78	4 US-09-513-999C-6923	Sequence 6923, Ap
16	54.5	26.7	2710	2 US-08-568-459A-12	Sequence 12, Appli
17	54.5	26.7	2710	2 US-08-487-826B-12	Sequence 12, Appli
18	54.5	26.7	2710	3 US-09-210-288-12	Sequence 12, Appli
19	54.5	26.7	3060	2 US-08-487-826B-14	Sequence 14, Appli
20	52.5	25.7	577	2 US-07-728-215-29	Sequence 29, Appli
21	52.5	25.7	577	3 US-08-938-085A-29	Sequence 29, Appli
22	52.5	25.7	577	4 US-10-072-844-29	Sequence 29, Appli
23	52.5	25.7	577	4 US-10-072-838-29	Sequence 29, Appli
24	52.5	25.7	577	4 US-10-072-841A-29	Sequence 29, Appli
25	52.5	25.7	577	4 US-10-219-631-29	Sequence 29, Appli
26	52.5	25.7	799	1 US-08-054-077C-2	Sequence 2, Appli
27	52	25.5	278	3 US-09-724-864-52	Sequence 52, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-845-583A-6  
; Sequence 6, Application US/09845583A  
; Patent No. 6635616  
; GENERAL INFORMATION:  
; APPLICANT: Burgeson, Robert  
; APPLICANT: Brunken, William Joseph  
; APPLICANT: Champlaud, Marie-France  
; APPLICANT: Hunter, Dale  
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF  
; FILE REFERENCE: 10287-056001  
; CURRENT APPLICATION NUMBER: US/09/845,583A  
; PRIOR FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 60/200,863  
; PRIOR FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 1799  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-845-583A-6

Query Match 29.4%; Score 60; DB 4; Length 1799;  
Best Local Similarity 29.8%; Pred. No. 31;  
Matches 14; Conservative 5; Mismatches 8; Indels 20; Gaps 3;

QY 5 YQKCHCHM-----GTHCHSSD-GRGVIPERPC 32  
DB 1111 FTGQCHCHAGFGGRTCSCQELYWCDPLGQCRACDCDPRG-IDKPC 1156

##### RESULT 2

US-08-896-449A-2  
; Sequence 2, Application US/08896449A  
; Patent No. 6040143  
; GENERAL INFORMATION:  
; APPLICANT: Venta, Patrick J  
; APPLICANT: Yuzbasiyan-Gurkan, Vilma  
; APPLICANT: Zschall, William D  
; APPLICANT: Brewer, George J  
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND  
; TITLE OF INVENTION: FACTOR AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
; STREET: 5445 Corporate Drive  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: USA

Sequence 27434, A  
Sequence 27804, A  
Sequence 21, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 47, Appl  
Sequence 133, App  
Sequence 47, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 2, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 24401, A  
Sequence 5, Appl  
Sequence 5, Appl

420 4 US-09-252-991A-27434  
470 4 US-09-252-991A-27804  
70 4 US-09-381-546-21  
207 3 US-08-974-022-47  
207 3 US-08-795-445A-47  
207 3 US-08-795-447A-47  
207 3 US-08-974-186-47  
207 3 US-08-795-446B-47  
207 3 US-08-706-945D-133  
207 4 US-08-577-788C-47  
207 1 US-08-292-549-2  
325 3 US-09-042-785A-9  
325 5 PCT-US91-02207-2  
298 3 US-09-080-044-9  
298 3 US-09-531-857A-9  
771 4 US-09-252-991A-24401  
277 1 US-08-690-457-5  
277 2 US-08-628-187-5

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43 24.8  
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45 24.5

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; ZIP: 48098
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,449A
; FILING DATE: 18-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REFERENCE/DOCKET NUMBER: 2115-001226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 248-641-1600
; TELEFAX: 248-641-0270
; TELEX: 287637
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2813 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-896-449A-2

Query Match      28.9%; Score 59; DB 3; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQOK-----CHCHMG-THCHSSDG-----PRGVIPBPRC 32
Db 710 YYDGEIQPEDIFSDHHTMTCYCEDGFNHCTTSGGLGSLLENPNVLSSPRC 758

RESULT 3
US-09-132-652-2
; Sequence 2, Application US/09132652
; Patent No. 6074932
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J.
; APPLICANT: Yuzbasiyan-Gurkan, Vilma
; APPLICANT: Schall, William D.
; APPLICANT: Brewer, George J.
; APPLICANT: Duffendeck, John
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: 2115S-001226CPB
; CURRENT APPLICATION NUMBER: US/09/132,652
; CURRENT FILING DATE: 1998-08-11
; EARLIER APPLICATION NUMBER: 08/896,449
; EARLIER FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-132-652-2

Query Match      28.9%; Score 59; DB 3; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQOK-----CHCHMG-THCHSSDG-----PRGVIPBPRC 32
Db 710 YYDGEIQPEDIFSDHHTMTCYCEDGFNHCTTSGGLGSLLENPNVLSSPRC 758

RESULT 4
US-09-886-900A-2
; Sequence 2, Application US/09886900A
; Patent No. 6767707
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon

```

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; APPLICANT: Venta, Patrick J.
; APPLICANT: Brewer, George J.
; APPLICANT: Vilma, Yuzbasiyan-Gurkan
; APPLICANT: Schall, William D.
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: UMV-1226CPPCUS
; CURRENT APPLICATION NUMBER: US/09/886,900A
; CURRENT FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US/09/662,478C
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/132,652
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: PCT/US99/18153
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-886-900A-2

Query Match      28.9%; Score 59; DB 4; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQOK-----CHCHMG-THCHSSDG-----PRGVIPBPRC 32
Db 710 YYDGEIQPEDIFSDHHTMTCYCEDGFNHCTTSGGLGSLLENPNVLSSPRC 758

RESULT 5
US-09-662-478C-2
; Sequence 2, Application US/09662478C
; Patent No. 6780583
; GENERAL INFORMATION:
; APPLICANT: Venta, Patrick J.
; APPLICANT: Brewer, George J.
; APPLICANT: Vilma, Yuzbasiyan-Gurkan
; APPLICANT: Schall, William D.
; TITLE OF INVENTION: DNA ENCODING CANINE VON WILLEBRAND FACTOR AND METHODS
; FILE REFERENCE: UMV-1226CPPCUS
; CURRENT APPLICATION NUMBER: US/09/662,478C
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/132,652
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: PCT/US99/18153
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-662-478C-2

Query Match      28.9%; Score 59; DB 4; Length 2813;
Best Local Similarity 30.6%; Pred. No. 66;
Matches 15; Conservative 4; Mismatches 10; Indels 20; Gaps 3;

QY 4 YYQOK-----CHCHMG-THCHSSDG-----PRGVIPBPRC 32
Db 710 YYDGEIQPEDIFSDHHTMTCYCEDGFNHCTTSGGLGSLLENPNVLSSPRC 758

RESULT 6
US-08-537-210A-1
; Sequence 1, Application US/08537210A
; Patent No. 5780300
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon

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RESULT 7
US-09-113-825-1
; Sequence 1, Application US/09113825
; Patent No. 6149902
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Fortini, Mark
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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1 OPERATING SYSTEM: DOS
2 SOFTWARE: FastSeq Version 2.0
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/113,825
5 FILING DATE:
6 CLASSIFICATION:
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 08/537,210
9 FILING DATE: 29-SEP-1995
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Mirock, S. Leslie
12 REGISTRATION NUMBER: 18,872
13 REFERENCE/DOCKET NUMBER: 7326-027
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 212-790-9090
16 TELEFAX: 212-869-8864
17 TELEX: 66141 PENNIE
18 INFORMATION FOR SEQ ID NO: 1:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 1015 amino acids
21 TYPE: amino acid
22 STRANDEDNESS:
23 TOPOLOGY: unknown
24 MOLECULE TYPE: protein
25 FEATURE:
26 NAME/KEY: hum N (Human No. 6149902ch 2)
27 LOCATION: 1155...2169
28 OTHER INFORMATION: Highly conserved ankyrin repeat
29 OTHER INFORMATION: region of No. 6149902ch
30 US-09-113-825-1
31
32 Query Match 28.7%; Score 58.5; DB 3; Length 1015;
33 Best Local Similarity 42.3%; Pred. No.:27;
34 Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
35
36 Qy 7 GKCHCHMGTHC-HSSDGPGRGVPEPR 31
37 | : | | | | | | | | | | | | |
38 Db 193 GQVKCRKGEQVHTASGPRCFCPSPR 218
39
40 RESULT 8
41 US-08-185-432-16
42 Sequence 16, Application US/08185432
43 Patent No. 5750652
44 GENERAL INFORMATION:
45 APPLICANT: Artavanis-Tsakonas, Spyridon
46 APPLICANT: Buseau, Isabelle
47 APPLICANT: Diederich, Robert J.
48 APPLICANT: Xu, Tian
49 APPLICANT: Matsuno, Kenji
50 TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
51 TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
52 NUMBER OF SEQUENCES: 23
53 CORRESPONDENCE ADDRESS:
54 ADDRESSEE: PENNIE & EDMONDS
55 STREET: 1155 Avenue of the Americas
56 CITY: New York
57 STATE: New York
58 COUNTRY: U.S.A.
59 ZIP: 10036-2711
60 COMPUTER READABLE FORM:
61 MEDIUM TYPE: Floppy disk
62 COMPUTER: IBM PC compatible
63 OPERATING SYSTEM: PC-DOS/MS-DOS
64 SOFTWARE: PatentIn Release #1.0, Version #1.30
65 CURRENT APPLICATION DATA:
66 APPLICATION NUMBER: US/08/185,432
67 FILING DATE: 21-JAN-1994
68 CLASSIFICATION: 530
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Mirock, S. Leslie
71 REGISTRATION NUMBER: 18,872
72 REFERENCE/DOCKET NUMBER: 7326-006

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/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2471 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/
US-08-185-432-16
/
Query Match 28.7%; Score 58.5; DB 1; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
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Qy 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 9
US-08-083-590A-19
/ Sequence 19, Application US/08083590A
/ Patent No. 5786158
/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, S. et al.
/ TITLE OF INVENTION: Therapeutic And Diagnostic Methods
/ TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
/ TITLE OF INVENTION: Nucleic Acids
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/083,590A
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/083,590
/ FILING DATE: 25-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7326-015
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 8698864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2471 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/
US-08-532-384-19
/
Query Match 28.7%; Score 58.5; DB 3; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
/
Qy 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 10
US-08-532-384-19
/ Sequence 19, Application US/08532384
/ Patent No. 6083904
/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, S. et al.
/ TITLE OF INVENTION: Therapeutic And Diagnostic Methods
/ TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
/ TITLE OF INVENTION: Nucleic Acids
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/532,384
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/083,590
/ FILING DATE: 25-JUN-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mistrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7326-015
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212 790-9090
/ TELEFAX: 212 8698864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2471 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/
US-08-532-384-19
/
Query Match 28.7%; Score 58.5; DB 3; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
/
Qy 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372

RESULT 11
US-08-899-232-1
/ Sequence 1, Application US/08899232
/ Patent No. 6436650
/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, Spyridon
/ APPLICANT: Oi. Huilin
/ TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
/ FILE REFERENCE: 7326-046
/ CURRENT APPLICATION NUMBER: US/08/899,232
/ CURRENT FILING DATE: 1997-07-23
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 2471
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-08-899-232-1
/
Query Match 28.7%; Score 58.5; DB 1; Length 2471;
Best Local Similarity 42.3%; Pred. No. 67;
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;
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Qy 7 GKCHCHMGTHC-HSSDGRGVPEPR 31
Db 1347 GQVKCRKGECVHTASGRFCFSPR 1372
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Query Match 28.7%; Score 58.5; DB 4; Length 2471;  
Best Local Similarity 42.3%; Pred. No. 67;  
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;  
QY 7 GKCHCHMGTHC-HSSDGRGVIPR 31  
Db 1347 GQVKCRKGEQCVHTASGRFCPSR 1372

RESULT 12  
US-09-121-457-1  
; Sequence 1, Application US/09121457  
; Patent No. 6692919  
; GENERAL INFORMATION:  
; APPLICANT: Artavanis-Tsakonas, S.  
; APPLICANT: Qi, H.  
; APPLICANT: Rand, M.  
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON  
; FILE REFERENCE: 7326-073  
; CURRENT APPLICATION NUMBER: US/09/121,457  
; CURRENT FILING DATE: 1998-07-23  
; EARLIER APPLICATION NUMBER: 08/899,232  
; EARLIER FILING DATE: 1997-07-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2471  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-121-457-1

Query Match 28.7%; Score 58.5; DB 4; Length 2471;  
Best Local Similarity 42.3%; Pred. No. 67;  
Matches 11; Conservative 3; Mismatches 11; Indels 1; Gaps 1;  
QY 7 GKCHCHMGTHC-HSSDGRGVIPR 31  
Db 1347 GQVKCRKGEQCVHTASGRFCPSR 1372

RESULT 13  
US-09-270-767-38503  
; Sequence 38503, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 38503  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-38503

Query Match 27.9%; Score 57; DB 4; Length 92;  
Best Local Similarity 41.2%; Pred. No. 3.7;  
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 7 GKCHCHMGTHCHSSDGP 23  
Db 27 GNCYCYLGSYCSRTFGP 43

RESULT 14  
US-09-270-767-53720  
; Sequence 53720, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:

; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 53720  
; LENGTH: 92  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-53720

Query Match 27.9%; Score 57; DB 4; Length 92;  
Best Local Similarity 41.2%; Pred. No. 3.7;  
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 7 GKCHCHMGTHCHSSDGP 23  
Db 27 GNCYCYLGSYCSRTFGP 43

RESULT 15  
US-09-513-999C-6923  
; Sequence 6923, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1998-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 6923  
; LENGTH: 78  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-513-999C-6923

Query Match 26.7%; Score 54.5; DB 4; Length 78;  
Best Local Similarity 29.1%; Pred. No. 6.4;  
Matches 16; Conservative 5; Mismatches 11; Indels 23; Gaps 4;  
QY 2 TVVYO-----GKCHC-----HMGTGC-----HSSDGRGV-----IPRCP 33  
Db 15 TTYVQHSQSPSCSPAHCPLRLTRHAGPLCLFTTSSNEAPRGLLWHPVPQLLCP 69

Search completed: November 16, 2004, 19:17:45  
Job time : 10.2785 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:40 ; Search time 3.10345 Seconds  
(without alignments)  
465.048 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPPIRTLEGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46.5	54.7	155	2 H97849	peptidoglycan-asso
2	46.5	54.7	155	2 F71637	peptidoglycan-asso
3	45	52.9	353	2 T01256	probable anthocyan
4	43	50.6	305	2 T36261	hypothetical prote
5	43	50.6	514	2 A49838	site-specific reco
6	43	50.6	514	2 A1988	fdxN element site-
7	43	50.6	687	2 AD2347	ribonuclease E (im
8	42	49.4	101	2 G75512	conserved hypotet
9	42	49.4	372	1 S28296	hypothetical prote
10	42	49.4	478	1 S60754	transcription fact
11	42	49.4	486	1 TVHUEG	transforming prote
12	42	49.4	535	2 S75159	hypothetical prote
13	42	49.4	1317	2 F83310	conserved hypotet
14	41.5	48.8	60	2 S68769	short neurotoxin -
15	41	48.2	272	2 S39641	flagellar motor ap
16	41	48.2	347	2 S71436	farnesyl-pyrophosp
17	41	48.2	368	2 S67507	morphogen lefty pr
18	41	48.2	368	2 C89840	conserved hypotet
19	41	48.2	597	2 T08681	adenosylhomocyste
20	41	48.2	788	2 AG0786	secreted effector
21	41	48.2	805	2 T24399	hypothetical prote
22	40	47.1	196	2 H64968	acetyl CoA acetyl
23	40	47.1	209	2 B83329	probable acyltrans
24	40	47.1	316	2 E75566	probable repressor
25	40	47.1	341	2 S43699	hypothetical prote
26	40	47.1	341	2 B35769	cAMP response elem
27	40	47.1	341	2 S03343	cAMP response elem
28	40	47.1	349	2 D75419	proline dipeptidas
29	40	47.1	396	2 E64049	cystathionine beta

#### ALIGNMENTS

##### RESULT 1

H97849

peptidoglycan-associated lipoprotein precursor [imported] - Rickettsia conorii (strain: C:Species: Rickettsia conorii)  
C:Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: H97849  
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R: Science 293, 2093-2098, 2001  
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A:Reference number: A97700; MUID:21442074; PMID:11557893  
A:Accession: H97849  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-155 <KUR>  
A:Cross-references: UNIPROT:Q92GC3; GB:AE006914; PIDN:AAU03738.1; PID:G15620330; GSPDB: C:Genetics:  
A:Gene: pal  
C:Superfamily: outer membrane protein A

Query Match 54.7%; Score 46.5; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 2.6;  
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 WVSQPPPIRTLEGSC 15

Db 74 WLSKHPEVKVTEGHC 89

##### RESULT 2

F71637

peptidoglycan-associated lipoprotein precursor (pal) RP771 - Rickettsia prowazekii  
C:Species: Rickettsia prowazekii  
C:Date: 21-Nov-1998 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: F71637  
R:Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alemark, Nature 396, 133-140, 1998  
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.  
A:Reference number: A71630; MUID:99039499; PMID:9823893  
A:Accession: F71637  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-155 <AND>  
A:Cross-references: UNIPROT:Q92CH2; GB:AJ235273; GB:AJ235269; NID:G3861237; PIDN:CAA151  
A:Experimental source: strain Madrid E  
C:Genetics:  
A:Gene: pal; RP771  
C:Superfamily: outer membrane protein A

Query Match 54.7%; Score 46.5; DB 2; Length 155;  
Best Local Similarity 50.0%; Pred. No. 2.6;  
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 WVSQPEIR-TLEGSC 15  
 Db 74 WLSKHPEVKVTVEGHC 89

RESULT 3  
 T01256  
 A:Title: probable anthocyanidin synthase [imported] - Arabidopsis thaliana  
 N:Alternate names: SRGI protein homolog F16M14.17  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
 C:Accession: T01256; F84802  
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, R.; Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, R.  
 A:Description: Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence.  
 A:Reference number: Z14213  
 A:Accession: T01256  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-353 <ROU>  
 A:Cross-references: UNIPROT:O80449; EMBL:AC003028; NID:G3335356; PID:G3335372  
 A:Experimental source: cultivar Columbia  
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
 A:Reference number: A84420; MUID:20083487; PMID:10617197  
 A:Accession: F84802  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-353 <STO>  
 A:Cross-references: GB:AE002093; NID:G3335372; PIDN:AAC27173.1; GSPDB:GN00139  
 C:Genetics:  
 A:Map position: 2  
 A:Introns: 160/2; 271/3  
 C:Superfamily: 1-aminocyclopropane-1-carboxylate oxidase

Query Match 52.9%; Score 45; DB 2; Length 353;  
 Best Local Similarity 72.7%; Pred. No. 11;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVSQPEIRTL 11  
 Db 152 WSPQPKIREL 162

RESULT 4  
 T36261  
 A:Title: hypothetical protein SCE68.11 - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 C:Accession: T36261  
 R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 A:Submitted to the EMBL Data Library, June 1999  
 A:Reference number: Z21576  
 A:Accession: T36261  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-305 <MUR>  
 A:Cross-references: UNIPROT:Q9WX21; EMBL:AL079345; PIDN:CAB45347.1; GSPDB:GN00070; SCOED  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOEDB:SCE68.11

Query Match 50.6%; Score 43; DB 2; Length 305;  
 Best Local Similarity 63.6%; Pred. No. 20;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVSQPEIRTL 11  
 Db 140 WVGPRPREVRL 150

RESULT 5  
 A49838  
 A:Title: site-specific recombinase XisF - Anabaena sp. (strain PCC 7120)  
 C:Species: Anabaena sp.  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 15-Oct-1999  
 C:Accession: A49838  
 R:Carasco, C.D.; Ramaswamy, K.S.; Ramasubramanian, T.S.; Golden, J.W.  
 A:Genes Dev. 8, 74-83, 1994  
 A:Title: Anabaena xisF gene encodes a developmentally regulated site-specific recombinase  
 A:Reference number: A49838; MUID:94116860; PMID:8288129  
 A:Accession: A49838  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-514 <CAR>  
 A:Cross-references: GB:L23220; NID:G349678; PIDN:AAA16762.1; PID:G349679  
 C:Genetics:  
 A:Gene: xisF

Query Match 50.6%; Score 43; DB 2; Length 514;  
 Best Local Similarity 53.8%; Pred. No. 33;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSPPEIRTEGSL 14  
 Db 414 VEPPEVKTLRAS 426

RESULT 6  
 AF1988  
 A:Title: fdxN element site-specific recombinase [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AF1988  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena Res. 8, 205-213, 2001  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AF1988  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-514 <KUR>  
 A:Cross-references: UNIPROT:Q8WY3; GB:BA000019; PIDN:BAE73414.1; PID:G17130804; GSPDB:G  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: xisF

Query Match 50.6%; Score 43; DB 2; Length 514;  
 Best Local Similarity 53.8%; Pred. No. 33;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VSPPEIRTEGSL 14  
 Db 414 VEPPEVKTLRAS 426

RESULT 7  
 AD2347  
 A:Title: ribonuclease E [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
 C:Accession: AD2347  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena Res. 8, 205-213, 2001  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AD2347  
 A:Status: preliminary



A;Molecule type: DNA  
A;Residues: 1-687 <KUR>  
A;Cross-references: UNIPROT:Q8YP69; GB:BA000019; PIDN:BA076030.1; PID:gl17133467; GSPDB:C  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr4331

Query Match 50.6%; Score 43; DB 2; Length 687;  
Best Local Similarity 72.7%; Pred. No. 44;  
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSQPPPIRTLE 12  
| : ||||| : |  
Db 560 VSEPPPIRTIVE 570

RESULT 8  
G75512  
conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: G75512  
R;White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: G75512  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-101 <WHI>  
A;Cross-references: UNIPROT:Q8R233; GB:AE001908; GB:AE000513; NID:96458174; PIDN:AAF1006  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR0492  
A;Map position: 1

Query Match 49.4%; Score 42; DB 2; Length 101;  
Best Local Similarity 41.7%; Pred. No. 9.4;  
Matches 5; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVSQPPPIRTLE 12  
| : ||||| : |  
Db 84 WLAEPQVSVLE 95

RESULT 9  
S28296  
hypothetical protein C40H1.1 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S28296  
R;Berke, M.  
submitted to the EMBL Data Library, December 1992  
A;Reference number: S28296  
A;Accession: S28296  
A;Molecule type: DNA  
A;Residues: 1-372 <BER>  
A;Cross-references: UNIPROT:Q03571; EMBL:Z19154; NID:96650; PID:96651  
C;Genetics:  
A;Introns: 72/1; 109/1; 139/2; 252/3; 324/3  
A;Superfamily: Caenorhabditis elegans hypothetical protein C40H1.1; ribonucleoprotein re  
F;59-139/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 49.4%; Score 42; DB 1; Length 372;  
Best Local Similarity 61.5%; Pred. No. 35;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 VSQPPPIRTLEGS 14  
| : ||||| : |  
Db 21 VSAPPEYKRLDGS 33

RESULT 10  
S60754  
transcription factor erg - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 27-Apr-1996 #sequence\_revision 23-May-1997 #text\_change 09-Jul-2004  
C;Accession: S60754  
R;Dhordain, P.; Dewitte, F.; Desbiers, X.; Stehelin, D.; Duterque-Cocquilland, M.  
Mech. Dev. 50, 17-28, 1995  
A;Title: Mesodermal expression of the chicken erg gene associated with precartilaginous  
A;Reference number: S60754; MUID:95329425; PMID:7605748  
A;Accession: S60754  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-478 <DHO>  
A;Cross-references: UNIPROT:Q90837; EMBL:X77159; NID:9790439; PIDN:CAA54404.1; PID:9790  
C;Genetics:  
A;Gene: erg  
A;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regul  
C;Keywords: DNA binding; phosphoprotein; proto-oncogene; transcription factor; transfor  
F;113-193/Domain: ets RII regulatory region homology <ETR>  
F;312-390/Domain: ets DNA-binding domain homology <ETS>

Query Match 49.4%; Score 42; DB 1; Length 478;  
Best Local Similarity 46.7%; Pred. No. 45;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 WVSQPPPIRTLEGSC 15  
| : ||||| : |  
Db 56 WLSQPPARVTIMEC 70

RESULT 11  
TVHUEG  
transforming protein erg-3 - human  
N;Contains: transforming protein erg-1; transforming protein erg-2  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1989 #sequence\_revision 30-May-1997 #text\_change 09-Jul-2004  
C;Accession: A94294; A94178; I58410; A28041; A29515  
R;Rao, V.N.; Papas, T.S.; Shyam, E.; Reddy, P.  
Science 237, 635-639, 1987  
A;Title: erg, a human ets-related gene on chromosome 21: alternative splicing, polyaden  
A;Reference number: A94294; MUID:87263429; PMID:3299708  
A;Accession: A94294  
A;Molecule type: mRNA  
A;Residues: 1-231,256-486 <REA>  
A;Cross-references: UNIPROT:P11308; UNIPROT:Q16113; GB:M17254; NID:9182186; PIDN:AAA523  
R;Reddy, E.S.P.; Rao, V.N.; Papas, T.S.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6131-6135, 1987  
A;Title: The erg gene: a human gene related to the ets oncogene.  
A;Reference number: A94178; MUID:87317608; PMID:33476934  
A;Accession: A94178  
A;Molecule type: mRNA  
A;Residues: 100-231,256-486 <REB>  
A;Cross-references: GB:M21535; NID:9182182; PIDN:AAA35811.1; PID:9182185  
R;Prasad, D.D.; Rao, V.N.; Lee, L.; Reddy, E.S.  
Oncogene 9, 669-673, 1994  
A;Title: Differentially spliced erg-3 product functions as a transcriptional activator.  
A;Reference number: I58410; MUID:94119611; PMID:8290279  
A;Accession: I58410  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: mRNA  
A;Residues: 230-259 <RES>  
A;Cross-references: GB:968130; NID:9544960; PIDN:AAB29724.1; PID:9544961  
C;Genetics:  
A;Gene: GDB:ERG  
A;Cross-references: GDB:119884; OMIM:165080  
A;Map position: 21q22.2-21q22.2  
C;Superfamily: transcription factor erg; ets DNA-binding domain homology; ets RII regul  
C;Keywords: alternative splicing; DNA binding; nucleus; proto-oncogene; transcrip f  
F;1-231,256-486/Product: transforming protein erg-2 #status predicted <EG2>  
F;100-231,256-486/Product: transforming protein erg-1 #status predicted <EG1>  
F;128-200/Domain: ets RII regulatory region homology <ETR>

F;320-398/Domain: ets DNA-binding domain homology <ETS>

Query Match 49.4%; Score 42; DB 1; Length 486;  
Best Local Similarity 46.7%; Pred. No. 46;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEGSC 15  
|:|||||:|  
Db 63 WLSQPPARVIRMEC 77

RESULT 12

S75159  
hypothetical protein sir1771 - *Synechocystis* sp. (strain PCC 6803)  
C;Species: *Synechocystis* sp.  
A;Variety: PCC 6803  
C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S75159  
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
s.  
A;Reference number: S74322; MUID:97061201; PMID:8905231  
A;Accession: S75159  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-535 <KAN>  
A;Cross-references: UNIPROT:P73052; EMBL:D90903; GB:AB001339; NID:G1652127; PIDN:BA11707  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.4%; Score 42; DB 2; Length 535;  
Best Local Similarity 85.7%; Pred. No. 50;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPE 7  
|:|||||  
Db 203 WISQPE 209

RESULT 13

F83310  
conserved hypothetical protein PA2684 [imported] - *Pseudomonas aeruginosa* (strain PA01)  
C;Species: *Pseudomonas aeruginosa*  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: F83310  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: F83310  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1317 <STO>  
A;Cross-references: UNIPROT:Q910F4; GB:AE004696; GB:AE004091; NID:G99498750; PIDN:AG0607  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA2684  
C;Superfamily: rhsF protein

Query Match 49.4%; Score 42; DB 2; Length 1317;  
Best Local Similarity 50.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEGSL 14  
|:|||||  
Db 155 WAAVPAELQTEGS 168

RESULT 14

S68769  
short neurotoxin - black-banded coral snake  
N;Alternate names: alpha-neurotoxin  
C;Species: *Micrurus nigrocinctus*  
C;Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C;Accession: S68769  
R;Rosso, J.P.; Vargas-Rosso, O.; Gutierrez, J.M.; Rochat, H.; Bougis, P.E.  
Eur. J. Biochem. 238, 231-239, 1996  
A;Title: Characterization of alpha-neurotoxin and phospholipase A(2) activities from *Mic*  
in from *Micrurus nigrocinctus nigrocinctus*.  
A;Reference number: S68769; MUID:96248443; PMID:8665942  
A;Accession: S68769  
A;Molecule type: protein  
A;Residues: 1-60 <ROS>  
A;Cross-references: UNIPROT:P80548  
A;Experimental source: *Micrurus nigrocinctus* (black-banded coral snake)  
C;Superfamily: snake toxin  
C;Keywords: neurotoxin; venom  
F;3-22,17-39,41-52,53-58/Disulfide bonds: #status predicted

Query Match 48.8%; Score 41.5; DB 2; Length 60;  
Best Local Similarity 64.3%; Pred. No. 6.8;  
Matches 9; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 3 SQPPEIRTL-EGSC 15  
|||||:|  
Db 9 SQPPTIKTCEGQC 22

RESULT 15

S39641  
flagellar motor apparatus homolog ytxD - *Bacillus subtilis*  
C;Species: *Bacillus subtilis*  
C;Date: 08-Jun-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S39641; B70003  
R;Grundy, F.J.; Waters, D.A.; Takova, T.Y.; Henkin, T.M.  
Mol. Microbiol. 10, 259-271, 1993  
A;Title: Identification of genes involved in utilization of acetate and acetoin in *Bacil*  
A;Reference number: S39641; MUID:95020526; PMID:7934817  
A;Accession: S39641  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-272 <GRU>  
A;Cross-references: UNIPROT:P39063; GB:U17309; NID:G661173; PIDN:AAA68282.1; PID:G348048  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Bruggliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Brington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Folger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, E.; Yoshikawa, H.; Danchin, A.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: B70003  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-272 <KUN>  
A;Cross-references: GB:Z99119; GB:AL009126; NID:G2635411; PIDN:CAB14951.1; PID:G2635457  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: ytxD  
C;Superfamily: flagellar motor rotation protein  
C;Keywords: transmembrane protein

Query Match 48.8%; Score 41; DB 2; Length 272;  
Best Local Similarity 42.9%; Pred. No. 37;  
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 WVSOPPEIRTEGS 14  
| | | | |  
Db 255 WQXQPKQVTKGS 268

Search completed: November 16, 2004, 19:15:59  
Job time : 6.10345 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 18:56:15 ; Search time 16.7507 Seconds  
(without alignments)  
515.240 Million cell updates/sec

Title: US-10-036-444-7  
Perfect score: 85  
Sequence: 1 WVSQPPERTLEGSC 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374546 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	89.4	176	1 NCT3 MACFA	P61483 macaca fasc
2	76	89.4	180	1 NCT3 MACMU	Q8mj02 macaca mula
3	76	89.4	201	1 NCT3_HUMAN	O14931 homo sapien
4	76	89.4	201	1 NCT3_PANTR	P61484 pan troglod
5	62	72.9	192	1 NCT3 RAT	Q8cfd9 rattus norv
6	49	57.6	2201	2 Q86NN1	Q86nn1 drosophila
7	49	57.6	2529	2 Q9VMC0	Q9vvc0 drosophila
8	48	56.5	1512	2 Q93HF2	Q93hf2 streptomyc
9	48	56.5	1517	2 Q82K7	Q82k7 streptomyc
10	47.5	55.9	155	2 Q7PSU5	Q7p9u5 rickettsia
11	46.5	54.7	155	2 Q9ZCH2	Q9zch2 rickettsia
12	46.5	54.7	155	2 Q92GC3	Q92gc3 rickettsia
13	46	54.1	236	2 Q9TCC7	Q9tcc7 nephroselm
14	46	54.1	397	2 Q84QL3	Q84ql3 oryza sativ
15	45	52.9	196	2 Q8H8H6	Q8h8h6 oryza sativ
16	45	52.9	353	2 Q80449	Q80449 arabidopsis
17	45	52.9	353	2 Q8LCL0	Q8lcl0 arabidopsis
18	44	51.8	304	2 Q73X58	Q73x58 mycobacteri
19	44	51.8	304	2 AAS04769	Aas04769 mycobacte
20	44	51.8	650	2 Q8FWS2	Q8fws2 brucella su
21	44	51.8	688	1 EOMD MOUSE	O54839 mus musculu
22	44	51.8	688	2 Q9JUL1	Q9j1l1 mus musculu
23	44	51.8	707	2 Q8BN22	Q8bn22 mus musculu
24	43.5	51.2	280	2 Q706L3	Q706l3 pseudomonas
25	43.5	51.2	280	2 CAE92937	Caes92937 pseudomon
26	43.5	51.2	804	2 Q8TEF5	Q8tef5 homo sapien
27	43	50.6	305	2 Q9WX21	Q9wx21 streptomyc
28	43	50.6	456	2 Q9W6Z9	Q9w6z9 xenopus lae
29	43	50.6	474	2 Q6ADU2	Q6adu2 salmonella
30	43	50.6	485	2 Q6GNZ9	Q6gnz9 xenopus lae
31	43	50.6	485	2 Q9W700	Q9w700 xenopus lae

32 43 50.6 514 2 Q44111  
33 43 50.6 514 2 Q8YVW3  
34 43 50.6 687 2 Q8YP69  
35 43 50.6 692 1 EOMD\_XENLA  
36 42 49.4 101 2 Q9RX23  
37 42 49.4 129 2 Q6ZSQ3  
38 42 49.4 129 2 BAC86894  
39 42 49.4 317 2 Q6XXK5  
40 42 49.4 317 2 AAP41719  
41 42 49.4 325 2 Q6XXK4  
42 42 49.4 325 2 AAP41720  
43 42 49.4 360 2 Q9D6W8  
44 42 49.4 372 1 YLF1\_CAEEL  
45 42 49.4 383 1 TRMU\_PASMU

## ALIGNMENTS

## RESULT 1

NCT3 MACFA  
ID NCT3 MACFA STANDARD; PRT; 176 AA.  
AC P61483; Q95JBB;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKP30) (NK-p30).  
DE cell p30-related protein) (NKP30) (NK-p30).  
GN Name=NCR3;  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lymphoid;  
RA Rizzi M., Biasoni R.;  
RT "Non MHC specific natural cytotoxicity receptors (NCR) expressed in Macaca fascicularis lymphoid cells.";  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; AJ278389; CAC41081.1; --  
CC HSP; F16410; I185.  
CC InterPro; IPR003599; IG.  
CC InterPro; IPR007110; IG-like.  
CC Pfam; PF00047; IG; 1.  
CC SMART; SM00409; IG; 1.  
CC PROSITE; PS50835; IG LIKE; 1.  
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.  
FT SIGNAL 1 18 Potential.  
FT CHAIN 19 176 Natural cytotoxicity triggering receptor  
FT DOMAIN 19 135 Extracellular (Potential).  
FT TRANSMEM 136 156 Potential.  
FT DOMAIN 157 176 Cytoplasmic (Potential).  
FT DOMAIN 19 126 IG-like.  
FT DISULFID 39 108 By similarity.

FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 176 AA; 19251 MW; 97B2A3B625E4AD54 CRC64;

Query Match 89.4%; Score 76; DB 1; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-05; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0;

QY 1 WVSQPEIRTELEGS 14  
 DB 20 WVSQPEIRTELEGS 33

RESULT 2  
 NCT3\_MACMU STANDARD; PRT; 180 AA.  
 AC Q8MJ02; Q8MJ01; Q95JB8;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
 GN Name=NCR3;  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
 RA LaBonte M.L., Miller J., Levin N.L.;  
 RT "Molecular cloning of rhesus monkey NKp46 and NKp30 and identification of NKp46SD and NKp30S.";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
 RC TISSUE=Lymphoid;  
 RA Rizzi M., Biassoni R.;  
 RT "NCR express by macaca NK cells.";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
 CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1;  
 CC IsoId=Q8MJ02-1; Sequence=VSP\_010414;  
 CC Note=No experimental confirmation available;  
 CC Name=2;  
 CC Note=No experimental confirmation available;  
 CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
 CC Note=No experimental confirmation available;  
 CC Name=3;  
 CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
 CC Note=No experimental confirmation available;  
 CC Name=4;  
 CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
 CC Note=No experimental confirmation available;  
 CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

-----  
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 -----

EMBL; AY035214; AAK63116.1; -;  
 EMBL; AY035215; AAK63117.1; -;  
 EMBL; AY035216; AAK63118.1; -;

DR EMBL; AY035217; AAK63119.1; -;  
 DR EMBL; AJ554301; CAD86942.1; -;  
 DR HSSP; P16410; 1185.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00409; Ig; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 KW Alternative splicing; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 18 Potential.  
 FT CHAIN 19 180 Natural cytotoxicity triggering receptor 3.  
 FT DOMAIN 19 133 Extracellular (Potential).  
 FT TRANSMEM 134 154 Potential.  
 FT DOMAIN 155 180 Cytoplasmic (Potential).  
 FT DOMAIN 19 126 Ig-like.  
 FT DISULFID 39 108 By similarity.  
 FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 121 121 N-linked (GlcNAc...) (Potential).  
 FT VARSPLIC 66 90 Missing (in isoform 2).  
 FT VARSPLIC 112 115 VLGL -> NILS (in isoform 3).  
 FT VARSPLIC 116 180 Missing (in isoform 3).  
 FT VARSPLIC 177 180 Missing (in isoform 4).  
 FT VARIANT 156 156 Missing (in isoform 4).  
 SQ SEQUENCE 180 AA; 19639 MW; 5C2DF53487B2A3B6 CRC64;  
 M -> V.

Query Match 89.4%; Score 76; DB 1; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 8e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTELEGS 14  
 DB 20 WVSQPEIRTELEGS 33

RESULT 3  
 NCT3\_HUMAN STANDARD; PRT; 201 AA.  
 AC Q14931; Q14930; Q14932; Q95667; Q95668; Q95669;  
 DT 05-JUL-2004 (Rel. 44, Created)  
 DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (NKp30) (NK-p30).  
 GN Name=NCR3; Synonyms=1C7;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, INTERACTION WITH CD32, AND FUNCTION.  
 RC TISSUE=Lymphoid;  
 RX PubMed=10562324;  
 RA Pende D., Parolini S., Pessino A., Sivori S., Augugliaro R., Morelli L., Marcenaro E., Accame L., Malaspina A., Biassoni R., Bottino C., Moretta L., Moretta A.;  
 RT "Identification and molecular characterization of NKp30, a novel triggering receptor involved in natural cytotoxicity mediated by human natural killer cells.";  
 RL J. Exp. Med. 190:1505-1516(1999).  
 [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND INTERACTION WITH CD32.  
 RC TISSUE=Peripheral blood;  
 RA Sato M., Yabe T., Ohashi J., Tsuchiya N., Hanaoka K., Tokunaga K., Juji T.;  
 RT "Identification of two novel single nucleotide polymorphisms in the

**Name=5; Synonyms=IC7f;**  
IsoId=014931-5; Sequence=VSP\_010411, VSP\_010413;  
Note-No experimental confirmation available;  
**Name=6; Synonyms=IC7d;**  
IsoId=014931-6; Sequence=VSP\_010411, VSP\_010412;  
Note-No experimental confirmation available;  
**-!- TISSUE SPECIFICITY:** Selectively expressed by all resting and activated NK cells and weakly expressed in spleen.  
**-!- SIMILARITY:** Belongs to natural cytotoxicity receptor (NCR) family.  
**-!- SIMILARITY:** Contains 1 immunoglobulin-like domain.

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EMBL; AJ223153; CAB54004.1; -  
EMBL; AB055881; BAB78472.1; -  
EMBL; Y14768; CAA75063.1; -  
EMBL; Y14768; CAA75064.1; -  
EMBL; Y14768; CAA75065.1; -  
EMBL; Y14768; CAA75066.1; -  
EMBL; Y14768; CAA75067.1; -  
EMBL; Y14768; CAA75068.1; -  
EMBL; AF031136; AAB86578.1; -  
EMBL; AF031137; AAB86579.1; -  
EMBL; AF031138; AAB86580.1; -  
EMBL; AF129756; AAD18088.1; -  
EMBL; AP000505; BAE63393.1; -  
EMBL; BC052582; AAH52582.1; -  
Genew; HGNC:19077; NCR3.  
GO; GO:0006955; P:immune response; NAS.  
GO; GO:0006954; P:inflammatory response; NAS.  
InterPro; IPR003599; IG.  
InterPro; IPR007110; IG-Like.  
Pfam; PF00047; IG; 1.  
SMART; SM00409; IG; 1.  
PROSITE; PS50835; IG\_LIKE; 1.  
Alternative splicing; Glycoprotein; Immunoglobulin domain; Receptor;  
Signal; Transmembrane.  
SIGNAL 1 18  
CHAIN 19 201  
Potential.  
Natural cytotoxicity triggering receptor  
3.  
Extracellular (Potential).  
Potential.  
Cytoplasmic (Potential).  
Ig-like.  
By similarity.  
N-linked (GlcNAc... ) (Potential).  
N-linked (GlcNAc... ) (Potential).  
Missing (in isoform 4, isoform 5 and isoform 6).  
FTID-VSP\_010411  
CLTWGERRQLPAVPAPLPFGSSAHLPPVPGG -> Y  
AKSTLSGFPLQ (in isoform 3 and isoform 6).  
FTID-VSP\_010412.  
LTWKGRRQLPAVPAPLPFGSSAHLPPVPGG -> HC  
HMGTCHSSDQGRGVPEPRCP (in isoform 2 and isoform 5).  
FTID-VSP\_010413  
FTID-VSP\_010414  
2855AE4D6902D429 CRC64;  
SEQUENCE 201 AA; 21593 MW; 2855AE4D6902D429 CRC64;  
Query Match 89.4%; Score 76; DB 1; Length 201;  
Best Local Similarity 100.0%; Pred.No. 9e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 WVSQPFEIRTEGS 14  
DB 20 WVSQPFEIRTEGS 33





```
RL Genome Res. 14:631-639(2004).
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to
CC the increased efficiency of activated natural killer (NK) cells to
CC mediate tumor cell lysis (By similarity).
CC -!- SUBUNIT: Interacts with CD32 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ430418; CAD23066.1; -.
CC DR EMBL; AJ430419; CAD23067.2; -.
CC DR EMBL; AJ430420; CAD23067.2; JOINED.
CC DR EMBL; AY273824; AAP13457.1; -.
CC DR EMBL; BX883046; CAB84000.1; -.
CC DR HSP; P09793; IDQT.
CC DR RGD; 727881; 1C7.
CC DR InterPro; IPR003599; Ig.
CC DR InterPro; IPR007110; Ig-like.
CC DR Pfam; PF00047; Ig; 1.
CC DR SMART; SM00409; IG_1.
CC DR PROSITE; PS00835; IG-LIKE; 1.
CC DR Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 18 Potential.
FT CHAIN 19 192 Natural cytotoxicity triggering receptor
FT FT 3.
FT DOMAIN 19 147 Extracellular (Potential).
FT TRANSMEM 148 168 Potential.
FT DOMAIN 169 192 Cytoplasmic (Potential).
FT DOMAIN 19 126 IG-like.
FT DISULFID 39 108 By similarity.
FT VARIANT 7 7 I -> V.
FT VARIANT 19 19 I -> V.
FT VARIANT 82 82 A -> V.
FT VARIANT 138 138 A -> T.
FT CONFLICT 135 135 A -> V (in Ref. 2).
SQ SEQUENCE 192 AA; 20470 MW; 7FC84FB252D22377 CRC64;

Query Match 72.98; Score 62; DB 1; Length 192;
Best Local Similarity 78.68; Pred. No. 0.023; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 2;

Qy 1 WVSQPPRTLEGS 14
Db 20 WVSQPPRTLEGS 33

RESULT 6
Q86NN1 PRELIMINARY; PRT; 2201 AA.
AC Q86NN1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE GH07949p (Fragment).
GN Names=CG11936; ORFNames=CG32529;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Eohydridea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
R1 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
R2 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
R3 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R4 Svirskas R., Tector C., Turner C., Turner E., Wang A.H., Wang X.,
R5 Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
R6 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
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RA Campe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT004503; AAO42667.1; -.
DR FlyBase; FBgn0052529; CG32529.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001025; BAH.
DR Pfam; PF01426; BAH; 1.
DR SMART; SM00439; BAH; 1.
FT NON_TER 1
SQ SEQUENCE 2201 AA; 237099 MW; 10303133A8B4864B CRC64;

Query Match 57.68; Score 49; DB 2; Length 2201;
Best Local Similarity 81.88; Pred. No. 54;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QPPEIRTLGDS 14
Db 340 QPPEIRTLGDS 350

RESULT 7
Q9VMCO PRELIMINARY; PRT; 2529 AA.
AC Q9VMCO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG32529-PA.
GN ORFNames=CG32529;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
R1 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
R2 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
R3 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R4 Svirskas R., Tector C., Turner C., Turner E., Wang A.H., Wang X.,
R5 Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
R6 Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
R7 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R8 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R9 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R10 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R11 Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
R12 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
R13 Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
R14 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R15 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R16 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
R17 Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
R18 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
R19 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R20 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R21 Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
R22 Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
R23 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
R24 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R25 Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
R26 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
R27 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
R28 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R29 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
R30 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
R31 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
R32 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
R33 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
R34 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
R35 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
R36 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R37 Svirskas R., Tector C., Turner C., Turner E., Wang A.H., Wang X.,
R38 Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
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RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL: AP005049; BAC74895.1; -.
DR GO: GO:0048037; Fc cofactor binding; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR009081; ACP like.
DR InterPro: IPR001227; Ac transferase.
DR InterPro: IPR002194; Chaperonin_TCP-1.
DR InterPro: IPR000794; Ketoacyl synth.
DR InterPro: IPR008268; Peptid_S16_AS.
DR InterPro: IPR006163; Pp bind.
DR Pfam: PF00109; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt; 1.
DR Pfam: PF00550; PP-binding; 1.
DR PROSITE: PS00075; ACP_DOMAIN; 1.
DR PROSITE: PS00606; B_KETOACYL SYNTHASE; 1.
DR PROSITE: PS01046; LON SER; UNKNOWN_1.
DR PROSITE: PS00995; TCPI_3; UNKNOWN_1.
KW Complete proteome; Transferase.
SQ SEQUENCE 1517 AA; 164167 MW; 43B0D4C75D48E962 CRC64;

Query Match 56.5%; Score 48; DB 2; Length 1517;
Best Local Similarity 61.5%; Pred. No. 55;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVSQPPEIR-TLEGSC 13
DB 944 WVEQPTARTVAG 956
ID Q7P9U5 PRELIMINARY; PRT; 155 AA.
AC Q7P9U5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Peptidoglycan-associated lipoprotein precursor.
GN Name: sibi of 907;
OS Rickettsia sibirica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=35793;
RN [1]
RP SEQUENCE FROM N.A.
RA Malek J.A., Ereneeveva M.E., Dasch G.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ompA family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABW0100001; EAA26095.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro: IPR006664; Bac_OmpA.
DR InterPro: IPR006665; OmpA_MotB.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OMPADOMAIN.
DR ProDom: PD000930; OmpA/MotB; 1.
KW Lipoprotein.
SQ SEQUENCE 155 AA; 17419 MW; 852EB9DC39B4C1E0 CRC64;

Query Match 55.9%; Score 47.5; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 6.2;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 WVSQPPEIR-TLEGSC 15

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DB 74 WLSXHPVKVTEGHC 89
ID Q9ZCH2 PRELIMINARY; PRT; 155 AA.
AC Q9ZCH2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN (Pal).
GN OrderedLocusNames=RE771;
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Madrid E;
RX MEDLINE=99039499; PubMed=9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sicheritz-Ponten T., Alismark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL: AJ235273; CAA15198.1; -.
DR PIR: F71637; F71637.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0009279; C: outer membrane (sensu Gram-negative Bacteria); IEA.
DR InterPro: IPR006664; Bac_OmpA.
DR InterPro: IPR006665; OmpA_MotB.
DR Pfam: PF00691; OmpA; 1.
DR PRINTS: PR01021; OMPADOMAIN.
DR ProDom: PD000930; OmpA/MotB; 1.
KW Complete proteome; Lipoprotein.
SQ SEQUENCE 155 AA; 17334 MW; D488CE6BEC40B8F CRC64;

Query Match 54.7%; Score 46.5; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 8; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 1 WVSQPPEIR-TLEGSC 15
DB 74 WLSXHPVKVTEGHC 89
ID Q9ZGC3 PRELIMINARY; PRT; 155 AA.
AC Q9ZGC3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Peptidoglycan-associated lipoprotein.
GN Name=pal; OrderedLocusNames=RC1200;
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
CC -!- SIMILARITY: Belongs to the ompA family.
DR EMBL: AE008667; AAL03738.1; -.

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 16, 2004, 17:12:10 ; Search time 15.9549 Seconds  
(without alignments)  
337.259 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPEIRTLBQSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	4	Aae02774 Human Nkp
2	85	100.0	15	8	Adq30927 Human Nkp
3	76	89.4	120	4	Aae02771 Human Nkp
4	76	89.4	120	8	Adq30924 Human Nkp
5	76	89.4	135	5	Aae19109 Human Nkp
6	76	89.4	177	2	Aay06402 Human B-C
7	76	89.4	190	2	Aay06401 Human B-C
8	76	89.4	190	4	Aae02769 Human Nkp
9	76	89.4	190	8	Ado19810 Human PRO
10	76	89.4	190	8	Adq30923 Human Nkp
11	76	89.4	201	2	Aay06403 Human B-C
12	76	89.4	369	5	Aae19110 Human Nkp
13	66	77.6	382	8	Adp48750 Human Nkp
14	49	57.6	1289	4	Abb70840 Drosophila
15	45.5	53.5	83	8	Abos8908 Human gen
16	45	52.9	164	4	Aau27977 Human con
17	45	52.9	301	3	Aag43485 Arabidops
18	45	52.9	353	3	Aag43484 Arabidops
19	45	52.9	353	5	Abb92033 Herbicida
20	45	52.9	380	4	Aag43483 Arabidops
21	44	51.8	185	3	Abg23939 Novel hum
22	44	51.8	688	3	Aay57393 Mouse ner
23	43.5	51.2	202	8	Adf69309 Human lun
24	43.5	51.2	211	8	Adf69308 Human lun
25	43	50.6	74	4	Aam88325 Human imm

26	43	50.6	276	4	ABG07919 Novel hum
27	43	50.6	303	8	ADP29234 Human sec
28	43	50.6	514	5	ABJ10466 XisF resc
29	42	49.4	63	5	ABP02197 Human ORF
30	42	49.4	134	3	AAg01336 Human sec
31	42	49.4	283	6	ABU39323 Protein e
32	42	49.4	451	2	AAy01520 Chicken C
33	42	49.4	459	6	ABP97695 Amino aci
34	42	49.4	462	5	AAU75313 Human Erg
35	42	49.4	462	6	ABU03476 Angiogene
36	42	49.4	462	6	ABU56566 Lung canc
37	42	49.4	462	7	ABD75275 Prostate
38	42	49.4	478	2	AAy01521 Chicken c
39	42	49.4	1128	7	ABO8286 Pseudomon
40	42	49.4	1317	4	AAU33622 Pseudomon
41	42	49.4	1317	6	ABU15571 Protein e
42	41.5	48.8	116	5	ABP42291 Human ova
43	41	48.2	87	5	ABP33534 Human ORF
44	41	48.2	137	5	AAU80378 Human DOP
45	41	48.2	149	4	ABG02616 Novel hum

ALIGNMENTS

RESULT 1

AAE02774

ID AAE02774 standard; peptide; 15 AA.

XX AC AAE02774;

XX AC AAE02774;

DT 06-AUG-2001 (first entry)

DE Human Nkp30 receptor immunogenic peptide for antiserum production.

XX Human; Nkp30 receptor; natural killer cell; cytostatic; antimicrobial;  
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;  
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;  
KW therapy.

XX Homo sapiens.

OS Homo sapiens.

XX WO200136630-A2.

PN 25-MAY-2001.

XX 15-NOV-2000; 2000WO-EP011697.

XX 15-NOV-1999; 99CA-02288307.

XX 15-NOV-1999; 99US-00440514.

XX (INNA-) INNATE PHARMA SAS.

XX (UYGE-) UNIV GENOVA.

XX Moretta A, Bottino C, Biassoni R;

XX WPI; 2001-329221/34.

XX NK cell compound, useful for detection and/or quantifying the presence of

XX NK cells, comprises the amino acid sequences of the Nkp30 molecule.

XX Claim 1; Page 33; 83pp; English.

XX The invention relates to human Nkp30 receptor and its corresponding cDNA molecule which is involved in natural cytotoxicity mediated by natural killer (NK) cells and antibodies that identify the same. Nkp30 receptor is a member of immunoglobulin super family (Ig-SF). Nkp30 is selectively expressed on the surface of human mature NK cells. Nkp30 and its cDNA are useful for detecting and/or quantifying the presence of NK cells in a biological sample. The invention also provide kits for detecting and/or quantifying the presence of NK cells, for the selective removal of NK cells from a biological sample, for the positive and selective purification of NK cells from a biological sample and for the in vitro



CC enhancement, graft versus host (GvH) inhibition, stimulation of graft  
CC versus tumour (GvT) and especially graft versus leukaemia (GvL), and for  
CC the prevention, palliation and/or therapy of solid or liquid tumours,  
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or  
CC microorganism, notably viral infection. NKp30 antibodies are useful for  
CC identifying NKp30 natural ligands and allow assessment of the level of  
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the  
CC comparison of this level to the standard physiological one. Hence NKp30  
CC antibodies are useful in the diagnosis of tumours or of infection. The  
CC present sequence is the extracellular region of human NKp30 receptor  
XX  
XX  
SQ Sequence 120 AA;

Query Match 89.4%; Score 76; DB 4; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

QY 1 WVSQPPEIRLTLEGS 14  
| | | | | | | | | | | | | |  
Db 2 WVSQPPEIRLTLEGS 15

RESULT 4  
ADQ30924  
ID ADQ30924 standard; protein; 120 AA.

XX AC ADQ30924;  
XX DT 23-SEP-2004 (first entry)  
XX DE Human NKp30 extracellular region.  
XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.

XX OS Homo sapiens.  
XX PN W02004056392-A1.

XX PD 08-JUL-2004.  
XX PF 22-DEC-2003; 2003WO-EP014716.

XX PR 23-DEC-2002; 2002US-0435344P.  
XX PA (INNA-) INNATE PHARMA.

XX PI Romagne F, Andre P;  
XX WP1; 2004-507595/48.

XX PT Pharmaceutical compositions that stimulate proliferation of natural  
PT killer cells useful for therapy of melanoma, chronic myeloid, and  
PT leukemia, comprise an anti-natural killer cell receptor antibody and  
PT interleukins.

XX PS Claim 3; SEQ ID NO 2; 35pp; English.

XX CC The present sequence is that of the extracellular region of human NKp30  
CC ADQ30923, a 190 amino acid polypeptide that is selectively expressed by  
CC natural killer (NK) cells, and particularly by mature NK cells. Claimed  
CC pharmaceutical compositions that have a stimulating effect on the  
CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
CC antibody(ies) and cytokine(s) being administered together or separately  
CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
CC antigen-binding fragment which specifically binds to NKp30 or to a  
CC fragment, including the extracellular region, of NKp30. The  
CC pharmaceutical compositions, when used for daily subcutaneous injection,  
CC comprising from 1 mg to 100 mg/Kg (body weight) of antibody(ies), and  
CC lower than 1 million units/square meters/day of cytokine(s), are useful  
CC for the prevention, palliation and therapy of e.g. melanoma, chronic  
CC myeloid leukaemia, acute myeloid leukaemia, lymphoma, multiple myeloma,

CC hepatocarcinoma, lung adenocarcinoma, neuroblastoma and for antimicrobial  
CC prevention, palliation and therapy (claimed).

XX SQ Sequence 120 AA;

Query Match 89.4%; Score 76; DB 8; Length 120;  
Best Local Similarity 100.0%; Pred. No. 0.00026; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

QY 1 WVSQPPEIRLTLEGS 14  
| | | | | | | | | | | | | |  
Db 2 WVSQPPEIRLTLEGS 15

RESULT 5

AAE19109  
ID AAE19109 standard; protein; 135 AA.

XX AC AAE19109;

XX DT 21-MAY-2002 (first entry)

XX DE Human NKp30 protein.

XX KW Human; natural killer cell activating protein; NKp46; therapy; virucide;  
KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;  
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; NKp30.

XX OS Homo sapiens.

XX PN W02000208287-A2.

XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-IL000664.

XX PR 20-JUL-2000; 2000IL-00137419.

XX PA (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
XX (UYNE ) UNIV BEN-GURION NEGEV.

XX PI Mandelboim O, Porgador A;

XX WP1; 2002-195870/25.

XX DR N-PSDB; AAD30466.

XX PT New targeting complex capable of targeting an active substance to a  
PT target cell, comprising a target recognition segment and an active  
PT segment, useful for treating pathologies associated with viral infections  
PT or cancer.

XX PS Example 1; Page 108; 113pp; English.

XX CC The invention relates to compositions and methods for the treatment and  
CC detection of a variety of viral infections, by using complex agents  
CC comprising the natural killer (NK) cells activating proteins, NKp46 and  
CC NKp44 and functional fragments thereof, linked to therapeutic or imaging  
CC agents. The complex is useful for treating pathologies associated with  
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein  
CC -Barr virus, cytomegalovirus, vaccinia virus, ECV, MVM or herpes virus)  
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for  
CC the imaging and monitoring of cancer. The complex may also be used to  
CC detect the presence of abnormal cells in a sample. The antibodies can be  
CC used to qualitatively or quantitatively detect the ligand for the  
CC complex. The present sequence is human NKp30 protein

XX SQ Sequence 135 AA;

Query Match 89.4%; Score 76; DB 5; Length 135;  
Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 0; Indels 0; Gaps 0;  
Matches 14; Conservative 0;

QY 1 WVSQPPEIRLTLEGS 14

Best Local Similarity 100.0%; Pred. No. 0.00038;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPPIRTLEGS 14  
Db 20 WVSQPPPIRTLEGS 33

RESULT 7  
AAY06401  
ID AAY06401 standard; protein; 190 AA.  
XX AC AAY06401;  
XX 20-SEP-1999 (first entry)  
XX Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
XX MBOG; B-cell myelin oligodendrocyte glycoprotein; human;  
KW signal transduction; immunomodulator; antiinflammatory;  
KW autoimmune disease; inflammation; gene therapy; diagnosis.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..12  
FT /note= "leader peptide"  
FT Protein 13..190  
FT /note= "mature protein"  
FT Modified-site 42  
FT /note= "N-glycosylated"  
FT Modified-site 68  
FT /note= "N-glycosylated"  
FT Modified-site 121  
FT /note= "N-glycosylated"  
FT Domain 139..162  
FT /note= "transmembrane domain"  
FT Peptide 166..177  
FT /note= "alternatively spliced C-terminal end"

XX WO9923867-A2.  
XX 20-MAY-1999.  
XX 05-NOV-1998; 98WO-US023826.  
XX 07-NOV-1997; 97US-0064761P.  
XX (BIOJ ) BIOGEN INC.  
XX Browning J;  
XX WPI; 1999-418423/35.  
XX N-PSDB; AAX59348.  
XX Novel B-cell myelin oligodendrocyte glycoproteins.  
XX Claim 2; Page 43; 43pp; English.

This sequence represents human BMOG, a novel member of the B cell myelin oligodendrocyte glycoprotein family that is expressed by germinal centre B cells. 3 C-terminal splice variants (see AAY06401-03) of BMOG were identified. The protein is present primarily in the spleen, in lymph nodes and in germinal centre B cells. It may have immunoregulatory functions, and soluble or chimeric fusion proteins of BMOG may be used to regulate the immune system in autoimmune or inflammatory disease. Vectors comprising BMOG, prokaryotic and eukaryotic host cells, and a method of producing BMOG using these transformed host cells are also provided. BMOG polypeptides can be used for modulating the immune system of a subject or to inhibit signal transduction in a cell expressing BMOG by contacting it with a soluble BMOG protein. The nucleic acid can be used for gene therapy. The protein can also be used to target a toxin, imaging agent or radionuclide to a cell expressing BMOG. (All claimed)

Query Match 89.4%; Score 76; DB 2; Length 177;



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XX SQ Sequence 190 AA;
Query Match 89.4%; Score 76; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPPIRTLEGS 14
   |||||
Db 20 WVSQPPPIRTLEGS 33

RESULT 8
AAE02769
ID AAE02769 standard; protein; 190 AA.
AC AAE02769;
XX
XX 06-AUG-2001 (first entry)
XX
XX Human NKp30 receptor.
DE
XX Human; NKp30 receptor; natural killer cell; cytostatic; antimicrobial;
KW melanoma; hepatocarcinoma; lung adenocarcinoma; viral infection; tumour;
KW immunosuppressant; antiviral; drug; grafting enhancement; leukaemia;
KW therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..18
FT /label= Signal_peptide
FT Protein 19..190
FT /label= Mature_NKp30_receptor_protein
FT Region 19..138
FT /label= Extracellular_region
FT /note= "Forms an immunoglobulin (Ig) V-like domain"
FT Modified-site 42
FT /note= "N-glycosylation site"
FT Modified-site 121
FT /note= "N-glycosylation site"
FT Region 139..157
FT /label= Transmembrane_region
FT Region 158..190
FT /label= Intracellular_region
XX
XX WO200136630-A2.
XX
XX 25-MAY-2001.
XX
XX 15-NOV-2000; 2000WO-EP011697.
XX
XX 15-NOV-1999; 99CA-02288307.
XX 15-NOV-1999; 99US-00448514.
XX
XX (INNA-) INNATE PHARMA SAS.
XX (UYGE-) UNIV GENOVA.
XX
XX Moretta A, Bottino C, Biassoni R;
XX
XX WPI; 2001-329221/34.
XX N-PSDB; AAD06564.
XX
XX Novel compound, useful for detection and/or quantifying the presence of
XX NK cells, comprises the amino acid sequences of the NKp30 molecule.
XX
XX Claim 1; Fig 7B; 83pp; English.
XX
XX The invention relates to human NKp30 receptor and its corresponding cDNA
XX molecule which is involved in natural cytotoxicity mediated by natural
XX killer (NK) cells and antibodies that identify the same. NKp30 receptor
XX is a member of immunoglobulin super family (Ig-SF). NKp30 is selectively
XX expressed on the surface of human mature NK cells. NKp30 and its cDNA are

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CC useful for detecting and/or quantifying the presence of NK cells in a
CC biological sample. The invention also provide kits for detecting and/or
CC quantifying the presence of NK cells, for the selective removal of NK
CC cells from a biological sample, for the positive and selective
CC purification of NK cells from a biological sample and for the in vitro
CC stimulation of NK cell cytotoxicity. The invention further provides a
CC pharmaceutical composition which is used as a drug for grafting
CC enhancement, graft versus host (GVH) inhibition, stimulation of graft
CC versus tumour (GVT) and especially graft versus leukaemia (GvL), and for
CC the prevention, palliation and/or therapy of solid or liquid tumours,
CC such as melanoma, hepatocarcinoma and lung adenocarcinoma, and/or
CC microorganism, notably viral infection. NKp30 antibodies are useful for
CC identifying NKp30 natural ligands and allow assessment of the level of
CC surface NKp30 ligand expressed on an NK-susceptible target cell and the
CC comparison of this level to the standard physiological one. Hence NKp30
CC antibodies are useful in the diagnosis of tumours or of infection. The
CC present sequence is human NKp30 receptor
XX
XX SQ Sequence 190 AA;

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Query Match 89.4%; Score 76; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 WVSQPPPIRTLEGS 14
   |||||
Db 20 WVSQPPPIRTLEGS 33

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RESULT 9
AD019810
ID AD019810 standard; protein; 190 AA.
XX
XX AC AD019810;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Human PRO polypeptide #367.
XX
XX KW Human; PRO; immune related disorder; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
XX systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
XX autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
XX diabetes mellitus; renal disease; demyelinating disease;
XX central nervous system; peripheral nervous system;
XX demyelinating polyneuropathy; Guillain-Barre syndrome;
XX chronic inflammatory demyelinating polyneuropathy.
XX
XX OS Homo sapiens.
XX
XX PN WO2004043361-A2.
XX
XX PD 27-MAY-2004.
XX
XX PF 06-NOV-2003; 2003WO-US035268.
XX
XX PR 08-NOV-2002; 2002US-0425235P.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Fong S, Dennis X, Clark H, Chiu H, Schoenfeld J, Williams PM;
XX PI Wood WL, Wu TD;
XX
XX DR WPI; 2004-420067/39.
XX DR N-PSDB; AD019809.
XX
XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
XX treating an immune related disorder such as systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
XX spondyloarthritis.
XX
XX Claim 7; SEQ ID NO 734; 1731pp; English.
XX
XX

```

CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The polypeptides and polynucleotides are useful for  
 CC treating and diagnosing immune related disorders in mammals. The immune  
 CC related disorders include systemic lupus erythematosus, rheumatoid  
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic  
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune  
 CC hemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes  
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the  
 CC central or peripheral nervous system, demyelinating polyneuropathy,  
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating  
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the  
 CC invention.

XX SQ Sequence 190 AA;  
 Query Match 89.4%; Score 76; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 0.00041;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPERTLEGS 14  
 |||||  
 DB 20 WVSQPPERTLEGS 33

## RESULT 10

ADQ30923  
 ID ADQ30923 standard; protein; 190 AA.

XX AC ADQ30923;  
 XX DT 23-SEP-2004 (first entry)  
 XX DE Human NKp30 polypeptide.  
 XX KW Natural killer cell; NK cell; NKp30; cytostatic; antimicrobial.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Region 19..138  
 FT /label= Extracellular region  
 FT /notes= "Region specifically described in Claim 3"  
 FT Region 20..133  
 FT /label  
 FT /notes= "Immunogenic peptide specifically described in  
 FT Claim 3"  
 FT Region 139..157  
 FT /label= Transmembrane region  
 FT /notes= "Region specifically described in Claim 3"  
 FT Region 158..190  
 FT /label= Cytoplasmic tail  
 FT /notes= "Region specifically described in Claim 3"

XX PN W02004056392-A1.

XX PD 08-JUL-2004.

XX XX 22-DEC-2003; 2003WO-EP014716.

XX PR 23-DEC-2002; 2002US-0435344P.

XX PA (INNA-) INNATE PHARMA.

XX PI Romagne F, Andre P;

XX DR WPI; 2004-507595/48.

XX XX Pharmaceutical compositions that stimulate proliferation of natural  
 PT killer cells useful for therapy of melanoma, chronic myeloid, and  
 PT leukemia, comprise an anti-natural killer cell receptor antibody and  
 PT interleukins.

XX PS Claim 3; SEQ ID NO 1; 35pp; English.

XX CC The present sequence is that of human NKp30, a 190 amino acid polypeptide  
 CC (about 30 kDa on SDS-PAGE) that is selectively expressed by natural  
 CC killer (NK) cells, and particularly by mature NK cells. Claimed  
 CC pharmaceutical compositions that have a stimulating effect on the  
 CC proliferation of NK cells comprise an antibody such as an anti-NKp30  
 CC antibody or anti-NKp46 antibody or its immuno-reactive fragment and a  
 CC cytokine selected from interleukin-2 (IL2), IL12, IL15 and IL21, the  
 CC antibody(ies) and cytokine(s) being administered together or separately  
 CC to a subject. The anti-NKp30 antibody is an isolated antibody or its  
 CC antigen-binding fragment which specifically binds to NKp30 or to a  
 CC fragment ADQ30924-ADQ30927 of NKp30. The pharmaceutical compositions,  
 CC when used for daily subcutaneous injection, comprising from 1 ng to 100  
 CC mg/kg (body weight) of antibody(ies), and lower than 1 million  
 CC units/square meters/day of cytokine(s), are useful for the prevention,  
 CC palliation and therapy of e.g. melanoma, chronic myeloid leukaemia, acute  
 CC myeloid leukaemia, lymphoma, multiple myeloma, hepatocarcinoma, lung  
 CC adenocarcinoma, neuroblastoma and for antimicrobial prevention,  
 CC palliation and therapy (claimed).

XX SQ Sequence 190 AA;

Query Match 89.4%; Score 76; DB 8; Length 190;  
 Best Local Similarity 100.0%; Pred. No. 0.00041;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPERTLEGS 14  
 |||||  
 DB 20 WVSQPPERTLEGS 33

## RESULT 11

AA06403  
 ID AA06403 standard; protein; 201 AA.

XX AC AA06403;  
 XX DT 20-SEP-1999 (first entry)  
 XX DE Human B-cell myelin oligodendrocyte glycoprotein BMOG.  
 XX KW BMOG; B-cell myelin oligodendrocyte glycoprotein; human;  
 KW signal transduction; immunomodulator; antiinflammatory;  
 KW autoimmune disease; inflammation; gene therapy; diagnosis.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 XX FT Peptide 1..12  
 FT /note= "leader peptide"  
 FT Protein 13..201  
 FT /note= "mature protein"  
 FT Modified-site 42  
 FT /note= "N-glycosylated"  
 FT Modified-site 68  
 FT /note= "N-glycosylated"  
 FT Modified-site 121  
 FT /note= "N-glycosylated"  
 FT Domain 139..162  
 FT /note= "transmembrane domain"  
 FT Peptide 166..201  
 FT /note= "alternatively spliced C-terminal end"

XX PN W09923867-A2.

XX PD 20-MAY-1999.

XX PF 05-NOV-1998; 98WO-US023826.

XX PR 07-NOV-1997; 97US-0064761P.

XX PA (BIOJ ) BIOGEN INC.

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PI Browning J;
XX
XX WPI; 1999-418423/35.
DR N-PSDB; AAX59349.
XX
XX Novel B-cell myelin oligodendrocyte glycoproteins.
PT
XX
XX Claim 2; Page 43; 43pp; English.
XX
XX This sequence represents human BMOG, a novel member of the B cell myelin
CC oligodendrocyte glycoprotein family that is expressed by germinal centre
CC B cells; 3 C-terminal splice variants (see AAY06401-03) of BMOG were
CC identified. The protein is present primarily in the spleen, in lymph
CC nodes and in germinal centre B cells. It may have immunoregulatory
CC functions, and soluble or chimeric fusion proteins of BMOG may be used to
CC regulate the immune system in autoimmune or inflammatory disease. Vectors
CC comprising BMOG, prokaryotic and eukaryotic host cells, and a method of
CC producing BMOG using these transformed host cells are also provided. BMOG
CC polypeptides can be used for modulating the immune system of a subject or
CC to inhibit signal transduction in a cell expressing BMOG by contacting it
CC with a soluble BMOG protein. The nucleic acid can be used for gene
CC therapy. The protein can also be used to target a toxin, imaging agent or
CC radionuclide to a cell expressing BMOG. (All claimed)
XX
XX Sequence 201 AA;
SQ
Query Match 89.4%; Score 76; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVSQPPPIRTLEGS 14
Db 20 WVSQPPPIRTLEGS 33
RESULT 12
AAE19110
ID AAE19110 standard; protein; 369 AA.
XX
XX AAE19110;
XX
XX 29-AUG-2003 (revised)
DT 21-MAY-2002 (first entry)
XX
XX Human Nkp30-IgG fusion protein.
DE
XX Human; natural killer cell activating protein; Nkp46; therapy; virucide;
KW viral infection; natural killer cell; NK; Nkp44; imaging agent; cancer;
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic; IgG;
KW immunoglobulin G; fusion protein.
XX
XX Homo sapiens.
OS
XX Chimeric.
XX
XX Key Location/Qualifiers
FH Region 1..135
FT /note= "Human Nkp30"
FT Region 136..369
FT /note= "Human IgG"
XX
XX WO200208287-A2.
XX
XX 31-JAN-2002.
PD
XX
XX 19-JUL-2001; 2001WO-ILC00664.
XX
XX 20-JUL-2000; 2000IL-00137419.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (UYNE ) UNIV BEN-GURION NEGEV.
XX
XX Mandelboim O, Porgador A;
PI
XX

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DR WPI; 2002-195870/25.
DR N-PSDB; AAD30467.
XX
XX New targeting complex capable of targeting an active substance to a
PT target cell, comprising a target recognition segment and an active
PT segment, useful for treating pathologies associated with viral infections
or cancer.
XX
XX Example 1; Page 108-110; 113pp; English.
XX
XX The invention relates to compositions and methods for the treatment and
CC detection of a variety of viral infections, by using complex agents
CC comprising the natural killer (NK) cells activating proteins, Nkp46 and
CC Nkp44 and functional fragments thereof, linked to therapeutic or imaging
CC agents. The complex is useful for treating pathologies associated with
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein
CC -Barr virus, cytomegalovirus, vaccinia virus, ECV, MVM or herpes virus)
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
CC the imaging and monitoring of cancer. The complex may also be used to
CC detect the presence of abnormal cells in a sample. The antibodies can be
CC used to qualitatively or quantitatively detect the ligand for the
CC complex. The present sequence is human Nkp30- immunoglobulin G (IgG) Fc
CC region fusion protein. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 369 AA;
SQ
Query Match 89.4%; Score 76; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WVSQPPPIRTLEGS 14
Db 20 WVSQPPPIRTLEGS 33
RESULT 13
ADP48750
ID ADP48750 standard; protein; 382 AA.
XX
XX ADP48750;
XX
XX 09-SEP-2004 (first entry)
DT
XX Human Nkp30-Fc conjugate protein SEQ ID NO:12.
DE
XX polypeptide conjugate; target recognition; natural killer cell receptor;
KW cytostatic; gene therapy; neoplastic disease; tumour; carcinoma;
KW squamous cell carcinoma; adenocarcinoma; small cell carcinoma; melanoma;
KW glioma; neuroblastoma; B cell lymphoma; T cell lymphoma; leukaemia;
KW human; natural killer cytotoxicity receptor conjugate;
KW Nkp30-Fc conjugate.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..25
FT /label= signal
FT Protein 26..382
FT /note= "Nkp30-Fc conjugate"
FT Misc-difference 26..31
FT /note= "Kpnl site"
FT Region 32..148
FT /label= Nkp30
FT Region 149..382
FT /label= Fc
XX
XX WO2004053054-A2.
XX
XX 24-JUN-2004.
PD
XX
XX 09-DEC-2003; 2003WO-IL001040.
XX
XX 09-DEC-2002; 2002US-0431728P.
PR

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XX PA (NATS-) NATSPEARS LTD.  
 XX FI Mandelboim O, Porgador A;  
 XX DR WPI; 2004-468830/44.  
 XX DR N-PSDB; ADP48757.  
 XX PT New polypeptide conjugate comprising a target recognition segment  
 XX PT comprising a Natural Killer cell receptor consisting of Nkp30, useful in  
 XX PT preparing a composition for treating a neoplastic disease.  
 XX PS Claim 5; SEQ ID NO 4; 66pp; English.  
 XX CC The present invention describes a polypeptide conjugate comprising: (a) a  
 CC target recognition segment comprising a natural killer cell receptor  
 CC (NCR) or its fragment consisting of Nkp30 or its fragment that binds to a  
 CC cellular ligand expressed on the surface of a target tumour cell; and (b)  
 CC a second segment comprising an active agent capable of exerting a  
 CC cytotoxic effect on the target cell. Also described: (1) an isolated  
 CC polynucleotide encoding the polypeptide conjugate; (2) a vector  
 CC comprising the polynucleotide; (3) a host cell comprising the vector and  
 CC capable of expressing the polypeptide conjugate; (4) a pharmaceutical  
 CC composition comprising the polypeptide conjugate and a carrier,  
 CC stabiliser or diluent; (5) treating a neoplastic disease in a subject;  
 CC (6) inhibiting the growth of a tumour in a subject; and (7) delivering a  
 CC cytotoxic substance to a target tumour cell in a subject. The polypeptide  
 CC conjugate has cytostatic activity, and can be used in gene therapy. The  
 CC polypeptide conjugate is useful in preparing a composition for treating a  
 CC neoplastic disease associated with a solid tumour or a non-solid tumour,  
 CC e.g., carcinoma, squamous cell carcinomas, adenocarcinomas, small cell  
 CC carcinomas, melanomas, gliomas, neuroblastomas, B cell lymphoma, T cell  
 CC lymphoma or leukaemia. The present sequence represents a human natural  
 CC killer cytotoxicity receptor conjugate, designated Nkp30-Fc conjugate,  
 CC which is used in the exemplification of the present invention.  
 XX SQ Sequence 382 AA;  
 Query Match 77.6%; Score 66; DB 6; Length 382;  
 Best Local Similarity 92.9%; Pred. No. 0.036; 1; Indels 0; Gaps 0;  
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 WVSQPPEIRTELEGS 14  
 Db 33 WVSQPLEIRTELEGS 46  
 RESULT 14  
 ABB70840  
 ID ABB70840 standard; protein; 1289 AA.  
 XX AC ABB70840;  
 XX DT 26-MAR-2002 (first entry)  
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 39312.  
 XX KW Drosophila; developmental biology; cell signalling; insecticide;  
 XX KW pharmaceutical.  
 XX OS Drosophila melanogaster.  
 XX FN WO200171042-A2.  
 XX PD 27-SEP-2001.  
 XX PF 23-MAR-2001; 2001WO-US009231.  
 XX PR 23-MAR-2000; 2000US-0191637P.  
 XX PR 11-JUL-2000; 2000US-00614150.  
 XX PA (PEXE ) PE CORP NY.  
 XX CC

PI Venter JC, Adams M, Li FWD, Myers EW;  
 XX WPI; 2001-656860/75.  
 DR N-PSDB; ABL14943.  
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 XX PT interactions.  
 XX PS Disclosure; SEQ ID NO 39312; 21pp + Sequence Listing; English.  
 XX CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737,  
 CC ABB72072). The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 1289 AA;  
 Query Match 57.6%; Score 49; DB 4; Length 1289;  
 Best Local Similarity 81.8%; Pred. No. 72;  
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 QPPRIETLEGS 14  
 Db 668 QPPRIETLEGS 678  
 RESULT 15  
 ABO58908  
 ID ABO58908 standard; protein; 83 AA.  
 XX AC ABO58908;  
 XX DT 29-JUL-2004 (first entry)  
 XX DE Human genome derived single exon protein #5142.  
 XX KW Human; gene expression; single exon probe; microarray;  
 XX KW alternative splicing event; genomic alteration.  
 XX OS Homo sapiens.  
 XX FN US2003194704-A1.  
 XX PD 16-OCT-2003.  
 XX PF 03-APR-2002; 2002US-00029386.  
 XX PR 03-APR-2002; 2002US-00029386.  
 XX PA (PENN/) PENN S G.  
 XX PA (RANK/) RANK D R.  
 XX PA (HANZ/) HANZEL D K.  
 XX FI Penn SG, Rank DR, Hanzel DK;  
 XX DR WPI; 2004-119264/12.  
 XX CC New human genome-derived single exon nucleic acid probes useful for human  
 XX PT gene expression analysis, for identifying or characterizing alternative  
 XX PT splicing events, for assessing genomic alterations or as tools for  
 XX PT surveying tissues.  
 XX PS Claim 45; SEQ ID NO 32542; 80pp; English.  
 XX CC The invention relates to a nucleic acid probe for measuring human gene  
 XX CC expression, comprising any of the 27,400 fully defined nucleotide

CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subscription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe protein of the invention. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPIO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
 CC  
 XX  
 SQ Sequence 83 AA;

Query Match 53.5%; Score 45.5; DB 8; Length 83;

Best Local Similarity 80.0%; Pred. No. 16;

Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 WVSQPPPIRTLEGSC 15  
 | : ||| : |||  
 Db 24 W-SRPPELRPWGSC 37

Search completed: November 16, 2004, 18:56:04  
 Job time : 18.9549 secs

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OM protein - protein search, using sw model

Run on: November 16, 2004, 19:14:52 ; Search time 13.4085 Seconds  
(without alignments)  
395.815 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPEIRTEGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 segs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
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2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	13	US-10-036-444-7
2	76	89.4	120	13	Sequence 7, Appli
3	76	89.4	135	15	Sequence 4, Appli
4	76	89.4	161	16	Sequence 17, Appl
5	76	89.4	177	16	Sequence 10, Appl
6	76	89.4	190	13	Sequence 5, Appli
7	76	89.4	190	13	Sequence 2, Appli
8	76	89.4	201	16	Sequence 4, Appli
9	76	89.4	369	13	Sequence 6, Appli
10	61.5	72.4	175	16	Sequence 18, Appl
11	61.5	72.4	185	16	Sequence 8, Appli
12	61.5	72.4	198	16	Sequence 7, Appli
13	50	58.8	71	15	Sequence 9, Appli

Sequence 146488,  
Sequence 14713, A  
Sequence 148764,  
Sequence 190212,  
Sequence 32542, A  
Sequence 168450,  
Sequence 195126,  
Sequence 192301,  
Sequence 59, Appl  
Sequence 193065,  
Sequence 236668,  
Sequence 193062,  
Sequence 43095, A  
Sequence 62747, A  
Sequence 2, Appli  
Sequence 1128, Ap  
Sequence 99, Appl  
Sequence 95, Appl  
Sequence 42, Appl  
Sequence 4, Appli  
Sequence 5118, Ap  
Sequence 43495, A  
Sequence 3423, Ap  
Sequence 158229,  
Sequence 60904, A  
Sequence 5014, Ap  
Sequence 220003,  
Sequence 2, Appli  
Sequence 5, Appli  
Sequence 229735,  
Sequence 341865,  
Sequence 16318, A

US-10-424-599-146488  
US-10-156-761-14713  
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US-09-864-408A-5014  
US-10-425-115-220003  
US-09-947-063-2  
US-10-425-115-229735  
US-10-425-115-341865  
US-10-369-493-16318

#### ALIGNMENTS

##### RESULT 1

US-10-036-444-7  
; Sequence 7, Application US/10036444  
; Publication No. US20020142445A1  
; GENERAL INFORMATION:  
; APPLICANT: INNATE PHARMA S.A.S.  
; TITLE OF INVENTION: "No. US20020142445A1 triggering receptor involved in natural  
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and  
; TITLE OF INVENTION: antibodies that identify the same"  
; FILE REFERENCE: SEQ-FR-1060  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/440,514  
; PRIOR FILING DATE: 1999-11-15  
; PRIOR APPLICATION NUMBER: 09/456,199  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:peptide derived  
; OTHER INFORMATION: from natural sequence, useful for antiserum  
; OTHER INFORMATION: production  
US-10-036-444-7

Query Match 100.0%; Score 85; DB 13; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.2e-06;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEGSC 15

DB 1 WVSQPEIRTEGSC 15

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RESULT 2
US-10-036-444-4
; Sequence 4, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-PR-1080
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-4

Query Match      89.4%; Score 76; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 2 WVSQPPEIRTEG 15

RESULT 3
US-10-333-481-17
; Sequence 17, Application US/10333481
; Publication No. US20040072256A1
; GENERAL INFORMATION:
; APPLICANT: Ofer Mandelboim
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC
; FILE REFERENCE: 68657
; CURRENT APPLICATION NUMBER: US/10/333,481
; CURRENT FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-333-481-17

Query Match      89.4%; Score 76; DB 15; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 4
US-10-696-259-10
; Sequence 10, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      89.4%; Score 76; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 5
US-10-696-259-5
; Sequence 5, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      89.4%; Score 76; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33

RESULT 6
US-10-036-444-2
; Sequence 2, Application US/10036444
; Publication No. US20020142445A1
; GENERAL INFORMATION:
; APPLICANT: INNATE PHARMA S.A.S.
; TITLE OF INVENTION: "No. US20020142445A1el triggering receptor involved in natural
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-5

Query Match      89.4%; Score 76; DB 16; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WVSQPPEIRTEG 14
Db 20 WVSQPPEIRTEG 33
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; TITLE OF INVENTION: cytotoxicity mediated by human Natural Killer cells and
; TITLE OF INVENTION: antibodies that identify the same"
; FILE REFERENCE: SEQ-FR-1060
; CURRENT APPLICATION NUMBER: US/10/036,444
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/440,514
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: 09/456,199
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Human NK cell
US-10-036-444-2

Query Match      89.4%; Score 76; DB 13; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
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Db      20 WVSQPPEIRLTLEGS 33

RESULT 7
US-10-696-259-4
; Sequence 4, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-4

Query Match      89.4%; Score 76; DB 16; Length 190;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 8
US-10-696-259-6
; Sequence 6, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US

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; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-6

Query Match      89.4%; Score 76; DB 16; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.00073;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
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Db      20 WVSQPPEIRLTLEGS 33

RESULT 9
US-10-333-481-18
; Sequence 18, Application US/10333481
; Publication No. US20040072256A1
; GENERAL INFORMATION:
; APPLICANT: Ofar Mandelboim
; APPLICANT: Angel Porgador
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSI
; FILE REFERENCE: 68657
; CURRENT APPLICATION NUMBER: US/10/333,481
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: PCT/IL01/00664
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 369
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-333-481-18

Query Match      89.4%; Score 76; DB 15; Length 369;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WVSQPPEIRLTLEGS 14
      |||||
Db      20 WVSQPPEIRLTLEGS 33

RESULT 10
US-10-696-259-8
; Sequence 8, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; FILE REFERENCE: A041 US

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; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-8

Query Match      72.4%; Score 61.5; DB 16; Length 175;
Best Local Similarity 92.9%; Pred. No. 0.12;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEGS 14
   |||||
Db 20 WVSQPEIRTEGS 32

RESULT 11
US-10-696-259-7
; Sequence 7, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-7

Query Match      72.4%; Score 61.5; DB 16; Length 185;
Best Local Similarity 92.9%; Pred. No. 0.13;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEGS 14
   |||||
Db 20 WVSQPEIRTEGS 32

RESULT 12
US-10-696-259-9
; Sequence 9, Application US/10696259
; Publication No. US20040110218A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC
; APPLICANT: BROWNING, Jeffrey
; TITLE OF INVENTION: BMOG, A Novel Protein Member of the
; TITLE OF INVENTION: Myelin-Oligodendrocyte Glycoprotein Family and Its Use for
; TITLE OF INVENTION: Immunomodulatory Purposes
; FILE REFERENCE: A041 US
; CURRENT APPLICATION NUMBER: US/10/696,259
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: US/09/560,855A
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: PCT/US98/23826
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/064761
; PRIOR FILING DATE: 1997-11-07

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-696-259-9

Query Match      72.4%; Score 61.5; DB 16; Length 198;
Best Local Similarity 92.9%; Pred. No. 0.14;
Matches 13; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WVSQPEIRTEGS 14
   |||||
Db 20 WVSQPEIRTEGS 32

RESULT 13
US-10-424-599-173742
; Sequence 173742, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 173742
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_127908C.1.pap
US-10-424-599-173742

Query Match      58.8%; Score 50; DB 15; Length 71;
Best Local Similarity 64.3%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 WVSQPEIRTEGS 14
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Db 8 WTPSPPHIREGS 21

RESULT 14
US-10-424-599-146488
; Sequence 146488, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146488
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(275)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
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Search completed: November 16, 2004, 19:45:08  
Job time : 14.4085 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (C) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 16, 2004, 19:04:36 ; Search time 4.21751 Seconds  
(without alignments)  
235.867 Million cell updates/sec

Title: US-10-036-444-7

Perfect score: 85

Sequence: 1 WVSQPPPIRTLEGSC 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

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- 4: /cgn2.6/prodata/1/iaa/6B-COMB.pep:\*
- 5: /cgn2.6/prodata/1/iaa/PTUS-COMB.pep:\*
- 6: /cgn2.6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	49.4	134	4 US-09-513-999C-5417	Sequence 5417, Ap
2	42	49.4	451	3 US-08-878-177-2	Sequence 2, Appli
3	42	49.4	478	3 US-08-878-177-4	Sequence 4, Appli
4	42	49.4	1128	4 US-09-252-991A-31032	Sequence 31032, A
5	41	48.2	170	4 US-09-270-767-36791	Sequence 36791, A
6	41	48.2	170	4 US-09-270-767-52008	Sequence 52008, A
7	41	48.2	249	3 US-09-189-760-6	Sequence 6, Appli
8	41	48.2	249	3 US-09-188-811-6	Sequence 6, Appli
9	41	48.2	249	3 US-09-514-422-6	Sequence 6, Appli
10	41	48.2	289	4 US-09-673-395A-155	Sequence 155, App
11	41	48.2	314	4 US-09-248-796A-17233	Sequence 17233, A
12	41	48.2	478	4 US-09-134-000C-6219	Sequence 6219, Ap
13	41	48.2	517	3 US-09-189-760-2	Sequence 2, Appli
14	41	48.2	517	3 US-09-514-422-2	Sequence 2, Appli
15	41	48.2	567	3 US-09-188-811-2	Sequence 2, Appli
16	40	47.1	84	4 US-09-135-238B-4	Sequence 4, Appli
17	40	47.1	196	4 US-09-492-709A-376	Sequence 376, App
18	40	47.1	202	4 US-09-328-352-5586	Sequence 5586, Ap
19	40	47.1	344	4 US-09-252-991A-31357	Sequence 31357, A
20	39	45.9	146	4 US-09-252-991A-32438	Sequence 32438, A
21	39	45.9	309	4 US-09-270-767-44392	Sequence 44392, A
22	39	45.9	650	4 US-09-489-039A-7678	Sequence 7678, Ap
23	39	45.9	788	4 US-09-248-796A-30511	Sequence 20511, A
24	38	44.7	353	4 US-09-252-991A-19842	Sequence 19842, A
25	38	44.7	409	1 US-08-190-802A-51	Sequence 51, Appli
26	38	44.7	409	2 US-08-283-917-3	Sequence 3, Appli
27	38	44.7	409	2 US-08-961-716-3	Sequence 3, Appli

Sequence 51, Appli  
Sequence 51, Appli  
Sequence 51, Appli  
Sequence 1119, Ap  
Sequence 9, Appli  
Sequence 9, Appli  
Sequence 7732, Ap  
Sequence 7982, Ap  
Sequence 1, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 387, App  
Sequence 387, App  
Sequence 387, App

ALIGNMENTS

RESULT 1

US-09-513-999C-5417  
; Sequence 5417, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513.999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5417  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 107  
; OTHER INFORMATION: Xaa=Ile or Met  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 108  
; OTHER INFORMATION: Xaa=Asp or Tyr  
US-09-513-999C-5417

Query Match 49.4%; Score 42; DB 4; Length 134;  
Best Local Similarity 46.7%; Pred. No. 23;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 WVSQPPPIRTLEGSC 15

Db 56 WLSQPPPIRTLEGSC 70

RESULT 2

US-08-878-177-2  
; Sequence 2, Application US/08878177  
; Patent No. 6294354  
; GENERAL INFORMATION:  
; APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwamoto et  
; TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes of  
; TITLE OF INVENTION: the Proteins  
; FILE REFERENCE: chugai seiyaku kabushiki kaisha 5001  
; CURRENT APPLICATION NUMBER: US/08/878.177



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; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-760-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 8
US-09-188-811-6
; Sequence 6, Application US/09188811
; Patent No. 6037148
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCES: THEREFOR
; FILE REFERENCES: MNI-046CP
; CURRENT APPLICATION NUMBER: US/09/188,811
; CURRENT FILING DATE: 1998-11-09
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-188-811-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 9
US-09-514-422-6
; Sequence 6, Application US/095:4422
; Patent No. 6291193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCES: THEREFOR
; FILE REFERENCES: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US/09/189,760
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-514-422-6

Query Match      48.2%; Score 41; DB 3; Length 249;
Best Local Similarity 35.7%; Pred. No. 65;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 14
Db      181 WIETPPSIKSLDSN 194

RESULT 10
US-09-673-395A-155
; Sequence 155, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-155

Query Match      48.2%; Score 41; DB 4; Length 289;
Best Local Similarity 46.7%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 WVSQPPEIRTELEGS 15
Db      267 WQQPPAARSCYGLC 281

RESULT 11
US-09-248-796A-17233
; Sequence 17233, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17233
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17233

Query Match      48.2%; Score 41; DB 4; Length 314;
Best Local Similarity 58.3%; Pred. No. 83;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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QY 1 WVSQPPERTLE 12
Db 302 WVNQPPTRKVE 313

RESULT 12
US-09-134-000C-6219
; Sequence 6219, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynd Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6219
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6219

Query Match 48.2%; Score 41; DB 4; Length 478;
Best Local Similarity 40.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 WVSQPPERTLE 15
Db 290 WIEMPPLELVGTC 304

RESULT 13
US-09-189-760-2
; Sequence 2, Application US/09189760
; Patent No. 6031078
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/189,760
; CURRENT FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/163,116
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/089,467
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: (PENDING)
; EARLIER FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-189-760-2

Query Match 48.2%; Score 41; DB 3; Length 517;
Best Local Similarity 35.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVSQPPERTLE 14
Db 449 WIETPPSIKSLDSN 462

RESULT 14
US-09-514-422-2
; Sequence 2, Application US/09514422
; Patent No. 62911193
; GENERAL INFORMATION:
; APPLICANT: Khodadoust, Mehran
; TITLE OF INVENTION: NOVEL MTBX PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MNI-046CP2
; CURRENT APPLICATION NUMBER: US/09/514,422
; CURRENT FILING DATE: 2000-02-28
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/163,116
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/089,467
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: (PENDING)
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-514-422-2

Query Match 48.2%; Score 41; DB 3; Length 517;
Best Local Similarity 35.7%; Pred. No. 1.4e+02;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 WVSQPPERTLE 14
Db 499 WIETPPSIKSLDSN 512

Search completed: November 16, 2004, 19:17:46
Job time : 5.21751 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2004, 00:10:44 ; Search time 39 Seconds  
(without alignments)  
468.748 Million cell updates/sec

Title: US-10-036-444-2  
Perfect score: 1020  
Sequence: 1 MAWMLLLILIMVPGSCALW.....GTHCHSSDGPVPIPEPRCP 190

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 96377

Minimum DB seq length: 0  
Maximum DB seq length: 190

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	118	11.6	136	2 B45893	T-cell receptor al
2	117.5	11.5	132	2 A24402	T-cell receptor al
3	116	11.4	146	2 S26408	T-cell receptor be
4	107.5	10.5	138	2 C27577	T-cell receptor al
5	106.5	10.4	131	2 D24092	T-cell receptor al
6	106.5	10.4	131	2 D24092	T-cell receptor al
7	106	10.4	132	1 RWSAV	T-cell receptor al
8	105	10.3	131	2 F45893	T-cell receptor al
9	104.5	10.2	132	2 S09713	Ig lambda chain pr
10	103	10.1	129	2 A42692	T-cell receptor al
11	102.5	10.0	110	2 B24092	T-cell receptor al
12	101.5	10.0	139	2 S36325	T-cell receptor de
13	101	9.9	120	2 I54487	T-cell receptor al
14	100	9.8	120	2 A24092	T-cell receptor al
15	99	9.7	130	2 A31211	T-cell receptor al
16	98.5	9.7	128	2 S24119	Ig lambda chain pr
17	98.5	9.7	152	2 S21826	T-cell receptor be
18	96	9.4	131	1 L6RUEB	Ig lambda chain pr
19	96	9.4	131	2 D24402	T-cell receptor al
20	95.5	9.4	140	2 PH0134	Ig lambda chain pr
21	94.5	9.3	108	2 JH0342	T-cell receptor al
22	94.5	9.3	186	2 S08614	cytotoxic T-lympho
23	93	9.1	117	2 I68824	T-cell receptor al
24	93	9.1	132	2 D45893	T-cell receptor al
25	92.5	9.1	136	2 S42510	ARM lambda protein
26	92.5	9.1	139	2 S36302	T-cell receptor de
27	92	9.0	129	2 A30554	Ig lambda chain pr
28	91.5	9.0	107	2 S60590	Ig heavy chain var
29	90.5	8.9	145	2 S21651	T-cell receptor be

30	90	8.8	132	2 A27632	T-cell receptor al
31	90	8.8	141	2 S38389	T-cell receptor be
32	89.5	8.8	113	2 S26266	T-cell receptor be
33	89.5	8.8	134	2 A45893	T-cell receptor al
34	89	8.7	137	2 C45893	T-cell receptor al
35	89	8.7	139	2 PH1225	Ig heavy chain pre
36	89	8.7	142	2 E28344	vpres protein prec
37	88.5	8.7	131	2 S24321	Ig lambda chain pr
38	88	8.6	147	2 PH0123	Ig heavy chain pre
39	87.5	8.6	111	2 JH0333	T-cell receptor al
40	87.5	8.6	132	2 S23374	T-cell receptor al
41	87	8.5	134	2 S03474	T-cell receptor al
42	86.5	8.5	95	2 G30603	T-cell receptor al
43	86.5	8.5	129	2 S03478	T-cell receptor al
44	86.5	8.5	136	2 S16848	Ig lambda chain V-
45	85.5	8.4	110	2 A49056	T-cell receptor al

ALIGNMENTS

RESULT 1

B45893  
T-cell receptor alpha chain precursor V region (BTA29) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: B45893  
R:Shinguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A:Reference number: A45893; MUID:90129157; PMID:2137108  
A:Accession: B45893  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <136>  
A:Cross-references: CB:D90011; NID:g217610; PIDN:BAAL4061.1; PID:g217611  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 11.6%; Score 118; DB 2; Length 136;  
Best Local Similarity 27.9%; Pred.No. 0.0017;  
Matches 41; Conservative 22; Mismatches 42; Indels 42; Gaps 9;

QY	4	MLLLILIMV-----HPGSCALWVQPPIRTILEGSAFLPCSFNAGQRLAIGSVTFW 56
DB	8	LLVILLASVDLEQPAEHSG-----ABPASLPVPEGAASLGCTYSDSNSLY----FTWY 57
QY	57	RDEVVPGKEVNGTPEP-----RGLAPLASSRFLHQAELHIRDVRGCHDASI 105
DB	58	RQ--YPGK-----GPEFLQVYANNKEGKFT--AQSNKTNKH-VSLRIRDSEPSDSAT 107
QY	106	YVCRVEVLGLVGVT-----GNGTRLVWE 128
DB	108	YLCAVDIISTTAGIKLTFGEGTRLIVK 134

RESULT 2

A24402  
T-cell receptor alpha chain precursor V region (CS) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 30-May-1997  
C:Accession: A24402  
R:Becker, D.M.; Patten, P.; Chien, Y.; Yokota, T.; Eshhar, Z.; Giedlin, M.; Gascoigne, Nature 317, 430-434, 1985  
A:Title: Variability and repertoire size of T-cell receptor V-alpha gene segments.  
A:Reference number: A93368; MUID:86014379; PMID:2995827  
A:Accession: A24402  
A:Molecule type: mRNA  
A:Residues: 1-132 <BEC>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 11.5%; Score 117.5; DB 2; Length 132;

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Best Local Similarity 30.8%; Pred. No. 0.0018;
Matches 44; Conservative 17; Mismatches 47; Indels 35; Gaps 9;

QY 12 VHPGSCALW-----VSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRDE 59
D 3 LHVSLVFLWLQGVSSQKXVQSPSLVPEGAMVSLNCFSDS-----ASQSIWYQOH 58
QY 60 VVPKQVR-----NGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEV 112
D 59 --PCKPKALISIFSGNKK-EGRLTVYLNASLH---VSLHKQSPSDSAVILCAVR 112

QY 113 LGLGVGT---GNCTRLVWEKEHP 132
D 113 SGANTGKLPFGHTILRV---HP 132

RESULT 3
S26408
T-cell receptor beta chain V region (5.5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26408
R: Bowman, S.J.; Lanchbury, J.S.
submitted to the EMBL Data Library, September 1992
A:Description: T cell receptor beta chain sequences from patients with rheumatoid arthritis
A:Reference number: S26408
A:Status: preliminary
A:Accession: S26408
A:Molecule type: mRNA
A:Residues: 1-146 <BOW>
A:Cross-references: EMBL:X68527; NID:G36172; PIDN:CAA48540.1; PID:G36173
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:35-112/Domain: immunoglobulin homology <IMM>

Query Match 11.4%; Score 116; DB 2; Length 146;
Best Local Similarity 26.5%; Pred. No. 0.0027;
Matches 39; Conservative 26; Mismatches 52; Indels 30; Gaps 7;

QY 1 MAMVLLILIMVHPGSCALWVSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRD 58
D 6 LCWVLLCLL---GAGSVETGVTOSPHLIKT-RGQVTLRCSSQSGH-----NTVSWYQQ 56
QY 59 EVVPG-----KEVRNGTPEFRGLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRV 110
D 57 ALCGGPOFIQYIRENG-----RGNFPFRGLQFPNYSSLENVNALELDDSDALYLCA 112

QY 111 EVLGLGVGT-----GNCTRLVWEKE 130
D 113 SPKGLGIPSGRYQYFGPGTRLVTVTD 139

RESULT 4
C27577
T-cell receptor alpha chain V region (5/10-20D) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C:Accession: C27577; C27557
R: Awamoto, A.; Ohashi, P.S.; Bircher, H.; Walker, C.L.; Michalopoulos, E.E.; Rupp, F.; H.
J. Exp. Med. 165, 591-600, 1987
A:Title: T cell receptor variable gene usage in a specific cytotoxic T cell response. PI
A:Reference number: A27557; MUID:87139812; PMID:3493320
A:Accession: C27577
A:Molecule type: mRNA
A:Residues: 1-138 <IWA>
A:Accession: C27557
A:Molecule type: mRNA
A:Residues: 22-138 <IW2>
A:Cross-references: EMBL:X05733
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 10.5%; Score 107.5; DB 2; Length 138;

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Best Local Similarity 31.9%; Pred. No. 0.015;
Matches 38; Conservative 17; Mismatches 45; Indels 19; Gaps 7;

QY 21 VSQPP-IRTLGSSAFPCSNASQGRLAIGSVTWFRDEVVPKQVR-----NGTPE 72
D 24 VQSPESLIVPEGAMTSLNCTFSDASQY----FAMYRQH--SGKAPKALMSIFSNGEKE 77
QY 73 FRRLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVL-GLGVGTGNGTRLVVEKE 130
D 78 -EGFTTHLKASLH---FSLHIRDSPSDSALYCAVSMTGKVKVFGSGTRLVSPD 132

RESULT 5
D24092
T-cell receptor alpha chain precursor V region (B10) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 01-Dec-2000 #text_change 11-Jan-2002
C:Accession: D24092; S03507
R: Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen receptor
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: D24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
R: Winoto, A.; Mjolsness, S.; Hood, L.
Nature 316, 832-836, 1985
A:Title: Genomic organization of the genes encoding mouse T-cell receptor alpha-chain.
A:Reference number: S03503; MUID:85296332; PMID:2993908
A:Accession: S03507
A:Molecule type: DNA
A:Residues: 111-130 <WIN>
A:Cross-references: EMBL:X03057; NID:G54519; PIDN:CAA26864.1; PID:gl334131
A:Note: This sequence was determined from the germline gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: T-cell receptor alpha chain V region B10 #status predicted <MAT>
F:36-109/Domain: immunoglobulin homology <IMM>

Query Match 10.4%; Score 106.5; DB 2; Length 131;
Best Local Similarity 29.6%; Pred. No. 0.017;
Matches 37; Conservative 19; Mismatches 42; Indels 27; Gaps 7;

QY 21 VSQPP-IRTL-EGSSAFPCSNASQGRLAIGSVTW----RDEVVPGKVRNGTPEFRG 75
D 24 VEQSPSALSUEGTGSGALRCNFTT-----MRAVQWFRKNSRGLNLFYLAGTKE-NG 77
QY 76 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLGVGTGNGTRLVVEKEHPQLG 135
D 78 RLKSAFDSK---ERYSTLHIRDAQLSDSGTYFCAAE-----ATSSGQKLV-----FG 131

QY 136 AGTVL 140
D 122 QGTVL 126

RESULT 6
D24092
T-cell receptor alpha chain precursor V region (4.C3) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C:Accession: D24092
R: Fink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.
Nature 321, 219-226, 1986
A:Title: Correlations between T-cell specificity and the structure of the antigen receptor
A:Reference number: A93380; MUID:86230843; PMID:3012351
A:Accession: D24092
A:Molecule type: mRNA
A:Residues: 1-131 <FIN>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor
F:1-20/Domain: signal sequence #status predicted <SIG>

```

RESULT 8  
F45893  
T-cell receptor alpha chain precursor V region (BTA25) - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 20-Jun-2000  
C:Accession: F45893  
R:Ishiguro, N.; Tanaka, A.; Shinagawa, M.  
Immunogenetics 31, 57-60, 1990  
A:Title: Sequence analysis of bovine T-cell receptor alpha chain.  
A:Reference number: F45893; UID:90129157; PMID:2137108  
A:Accession: F45893  
A>Status: preliminary

```

RESULT 10
A42692
T-cell receptor alpha chain (lysozyme peptide specific) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A42692
R:Kobori, J.A.; Hood, L.; Shastri, N.
Proc. Natl. Acad. Sci. U.S.A. 89, 2940-2944, 1992
A:Title: Structure-function relationship among T-cell receptors specific for lysozyme f
A:Reference number: A42692; MUID:92212944; PMID:1313573
A:Accession: A42692
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <KOB>
A:Cross-references: GB:M87844; NID:G201804; PIDR:AA51236.1; PID:9554375
A:Experimental source: T-cell hybrid BO4H.9.1
A:Note: sequence extracted from NCBI backbone (NCBIN:92850. NCBIP:92851)

```

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;35-109/Domain: immunoglobulin homology <IMM>

Query Match 10.1%; Score 103; DB 2; Length 129;  
Best Local Similarity 29.8%; Pred. No. 0.035;  
Matches 39; Conservative 14; Mismatches 34; Indels 44; Gaps 8;

QY 20 WVS-----QPPBIRTESSAFPCSFNASQGLAIGSVTFRDB-----VYPG 63  
DB 18 WSGDKVKQSPSALSQEGTNSALRCNFS-----IAATVQWFLQNGSLINLILYLP- 71  
QY 64 KEVRNGTPEFRGRAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGSGVTGN-- 121  
DB 72 -----GTKE-NGRLKSAFDSK---ESYSTLHIRDAQLEDSTGYFCAAE-----DTGNVYK 116  
QY 122 -----GTRLVY 127  
DB 117 YVEGAGTRLVKV 127

## RESULT 11

B24092  
T-cell receptor alpha chain V region (5C.C7) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C;Accession: B24092  
R;Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A;Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A;Reference number: A93380; MUID:86230843; PMID:3012351  
A;Accession: B24092  
A;Molecule type: mRNA  
A;Residues: 1-110 <FIN>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 102.5; DB 2; Length 110;  
Best Local Similarity 31.9%; Pred. No. 0.033;  
Matches 36; Conservative 16; Mismatches 46; Indels 15; Gaps 6;

QY 21 VSQPPBIRTL-EGSSAFPCSFNASQGLAIGSVTFW----RDEVVPGKEVRNGTPEFRG 75  
DB 4 VEQSPSALSJHEGTDSALRCNFTTT-----MRVQWFRKNRSGSLINLYLASGTKE-NG 57  
QY 76 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGLG-VGTGNGTRLVY 127  
DB 58 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAAEASNTNKVFGTGLQV 107

## RESULT 12

S36325  
T-cell receptor delta chain precursor - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 21-Jan-2000  
C;Accession: S36325; S23040  
R;Hein, W.R.; Dudley, L.  
EMBO J. 12, 715-724, 1993  
A;Title: Divergent evolution of T cell repertoires: extensive diversity and development  
A;Reference number: S36287; MUID:93178447; PMID:8440261  
A;Accession: S36325  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-139 <HEI>  
A;Cross-references: EMBL:Z12997; NID:G2258; PIDN:CAA78341.1; PID:G2259  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;33-113/Domain: immunoglobulin homology <IMM>

Query Match 10.0%; Score 101.5; DB 2; Length 139;  
Best Local Similarity 29.7%; Pred. No. 0.052;  
Matches 41; Conservative 14; Mismatches 60; Indels 23; Gaps 7;

QY 9 LIMVHPGSCALWVSQ-PPEIRTEGSSAFPCSFNASQGLAIGSVTFWR---DEVVPGK 64  
DB 9 LLIFYKGLVLCNQVTQSSPEQVRVASGREVTLCQTFQITYSN---PDLYWYRKTPDAVFQFV 65  
QY 65 EVANGTPEFRGRAPLASSRFLHDHQA-----ELHIRDVRGHDASIVYCRVEVLGSGV-- 117  
DB 66 LYRDNT---RSRDADFARGFTVQHSVRSKTFELVSSVRPEDTATYYCALD-LQRGIVYD 121  
QY 118 -----GTGNGTRLVWKE 130  
DB 122 TTDKLFEGKTRLIVEPE 139

## RESULT 13

I54487  
T-cell receptor alpha chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I54487; I68823  
R;Nakajima, P.B.; Di Vincenzo, J.P.; Jameson, S.C.; Gascoigne, N.R.J.  
Immunogenetics 35, 190-198, 1992  
A;Title: Chromosome 14 in B10.A (18R) mice is recombinant and includes Tera-V alleles.  
A;Reference number: I54487; MUID:92165347; PMID:1371499  
A;Accession: I54487  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-120 <RES>  
A;Cross-references: UNIPROT:Q31213; GB:M55634; NID:G199677; PIDN:AAA39701.1; PID:G199678  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 104-120 <RE2>  
A;Cross-references: GB:M55634; NID:G199677; PIDN:AAA39702.1; PID:G199679  
A;Note: J-alpha TA61  
C;Genetics:  
A;Gene: MHC-V-alpha-11; J-alpha-TA61  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: transmembrane protein  
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 9.9%; Score 101; DB 2; Length 120;  
Best Local Similarity 31.6%; Pred. No. 0.049;  
Matches 36; Conservative 17; Mismatches 47; Indels 14; Gaps 6;

QY 21 VSQPPBIRTL-EGSSAFPCSFNASQGLAIGSVTFWRD-----EVVPGKEVRNGTPEFRG 75  
DB 14 VEQSPSALSJHEGTDSALRCNFTTT-----MRSVQWFRKNRSGSLISLYLASGTKE-NG 67  
QY 76 RLAPLASSRFLHDHQAELHIRDVRGHDASIVYCRVEVLGSGVT-GNGTRLVVE 128  
DB 68 RLKSAFDSK---ERYSTLHIRDAQLEDSTGYFCAADNTNGLTTFGDTVLTVK 119

## RESULT 14

A24092  
T-cell receptor alpha chain V region (C.F6) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 21-Jan-2000  
C;Accession: A24092  
R;Pink, P.J.; Matis, L.A.; McElligott, D.L.; Bookman, M.; Hedrick, S.M.  
Nature 321, 219-226, 1986  
A;Title: Correlations between T-cell specificity and the structure of the antigen receptor  
A;Reference number: A93380; MUID:86230843; PMID:3012351  
A;Accession: A24092  
A;Molecule type: mRNA  
A;Residues: 1-110 <FIN>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: T-cell receptor  
F;16-89/Domain: immunoglobulin homology <IMM>

Query Match 9.8%; Score 100; DB 2; Length 110;  
Best Local Similarity 28.8%; Pred. No. 0.055;

Search completed: November 17, 2004, 00:20:13  
Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 00:02:59 ; Search time 191 Seconds  
(without alignments)  
572.362 Million cell updates/sec

Title: US-10-036-444-2

Perfect score: 1020

Sequence: 1 MAMULLLIILMHVPGSCALW.....GTHCHSDGPRGVPEPRCP 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 707533

Minimum DB seq length: 0

Maximum DB seq length: 190

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	916	89.8	180	1 NCT3_MACMU	Q8MJ02 macaca mula
2	896	87.8	176	1 NCT3_MACFA	P61483 macaca fasc
3	109	10.7	172	2 Q71AW3	Q71AW3 bos taurus
4	109	10.7	172	2 AAQ10930	AAQ10930 bos taurus
5	106	10.4	132	1 TVA2_MOUSE	P01739 mus musculus
6	104	10.2	174	2 Q921A7	Q921A7 rattus norv
7	102.5	10.0	164	2 Q90XW9	Q90XW9 orectolobus
8	100	9.8	160	2 Q8TDA6	Q8TDA6 homo sapien
9	98.5	9.7	152	2 Q6LBN1	Q6LBN1 homo sapien
10	98.5	9.7	152	2 CAA39607	CAA39607 homo sapi
11	96	9.4	131	1 LV6E_HUMAN	P06319 homo sapien
12	95.5	9.4	164	2 Q90XX2	Q90XX2 orectolobus
13	91.5	9.0	108	2 Q8J25	Q8J25 orectolobus
14	91	8.9	167	2 BAC05245	BAC05245 homo sapi
15	90	8.8	178	2 Q9DJU4	Q9DJU4 mus musculus
16	89.5	8.8	137	2 Q95653	Q95653 homo sapien
17	89	8.7	142	1 VPR2_MOUSE	P13373 mus musculus
18	88.5	8.7	132	2 Q8TBD0	Q8TBD0 homo sapien
19	88	8.6	148	2 Q6PU28	Q6PU28 homo sapien
20	88	8.6	148	2 AAH23973	AAH23973 homo sapi
21	88	8.6	179	2 Q921X1	Q921X1 mus musculus
22	87.5	8.6	141	2 Q9NU66	Q9NU66 homo sapien
23	87.5	8.6	176	2 Q9NU65	Q9NU65 homo sapien
24	87.5	8.6	183	2 Q9NU64	Q9NU64 homo sapien
25	87	8.5	189	2 BAC86223	BAC86223 homo sapi
26	86.5	8.5	182	2 Q6JXL8	Q6JXL8 homo sapien
27	86.5	8.5	182	2 Q6X1E7	Q6X1E7 orectolobus
28	86	8.4	111	2 AAP49001	AAP49001 homo sapi
29	86	8.4	111	2 AAP86761	AAP86761 orectolob
30	85.5	8.4	115	2 Q9B2K2	Q9B2K2 homo sapien
31	85	8.3	164	2 Q99KG0	Q99KG0 mus musculus

32 84 8.2 133 1 TVB2\_HUMAN  
33 83.5 8.2 135 2 Q90542  
34 83.5 8.2 164 2 Q90XW7  
35 83 8.1 134 1 TVB7\_MOUSE  
36 82.5 8.1 167 2 Q90XX1  
37 82 8.0 155 2 Q8TWK2  
38 82 8.0 167 2 Q90XW8  
39 80.5 7.9 142 2 Q9YHF2  
40 80 7.8 120 2 BAC00300  
41 80 7.8 142 1 VPR1\_MOUSE  
42 80 7.8 142 2 BAB27218  
43 80 7.8 142 2 BAB27242  
44 79.5 7.8 112 2 Q96JD2  
45 79.5 7.8 130 1 LV1G\_HUMAN

#### ALIGNMENTS

##### RESULT 1

NCT3\_MACMU  
ID NCT3\_MACMU STANDARD; PRT; 180 AA.  
AC Q8MJ02; Q8MJ00; Q8MJ01; Q95JB8;  
DT 05-JUL-2004 (Rel. 44, Created)  
DT 05-JUL-2004 (Rel. 44, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Natural cytotoxicity triggering receptor 3 precursor (Natural killer cell p30-related protein) (Nkp30) (NK-p30).  
DE cell p30-related protein) (Nkp30) (NK-p30).  
GN Name=NCR3;  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9544;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT VAL-156.  
RA LaBonte M.L., Miller J., Letvin N.L.;  
RT "Molecular cloning of rhesus monkey Nkp46 and NKp30 and identification of NKp46SD and NKp30S.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 4), AND VARIANT VAL-156.  
RC TISSUE=Lymphoid;  
RT Rizzi M., Biassoni R.;  
RA "NCR express by macaca NK cells.";  
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).  
CC -!- SUBUNIT: Interacts with CD32 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=4;  
CC Name=1;  
CC IsoId=Q8MJ02-1; Sequence=Displayed;  
CC Note=No experimental confirmation available;  
CC Name=2;  
CC IsoId=Q8MJ02-2; Sequence=VSP\_010414;  
CC Note=No experimental confirmation available;  
CC Name=3;  
CC IsoId=Q8MJ02-3; Sequence=VSP\_010415, VSP\_010416;  
CC Note=No experimental confirmation available;  
CC Name=4;  
CC IsoId=Q8MJ02-4; Sequence=VSP\_010417;  
CC Note=No experimental confirmation available;  
CC -!- SIMILARITY: Belongs to natural cytotoxicity receptor (NCR) family.  
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial





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DE EMBL: AF539438; AAQ10930.1; -
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;

Query Match 10.7%; Score 109; DB 2; Length 172;
Best Local Similarity 25.6%; Pred. No. 0.088;
Matches 43; Conservative 22; Mismatches 69; Indels 34; Gaps 5;

QY 6 LLILIMVHPSGSCALWVSQPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEVVPGKE 65
DB 23 LFFLVTFPVFSKGMNVTQPPVLASSRGVASFCEYESS-GRADVRVTVLREAGSQVTE 81
QY 66 VRNGTPEFRGLAPLASSRFL--HDHQAEHLHVRDGHDSIYVCRVEVL--GLGVGT 119
DB 82 VCAGTYVDELFDDSTCIGTSRGKNKNTLTIQGLRAMDTGLYCKVELMYPPIYVGI 141
QY 120 GNGTRL-VVEKEHPQLGAGTVLLLRAGFVAVSFLSVAGSTVYVQKGC 166
DB 142 GNGTQIVYIAKEK-----KPSYIRGLC 163

RESULT 4
AAQ10930 PRELIMINARY; PRT; 172 AA.
ID AAQ10930;
AC AAQ10930;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE CTLA-4 isoform 1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Ann J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539438; AAQ10930.1; -
SQ SEQUENCE 172 AA; 18972 MW; 7F53F5928EFA39E4 CRC64;

Query Match 10.7%; Score 109; DB 2; Length 172;
Best Local Similarity 25.6%; Pred. No. 0.088;
Matches 43; Conservative 22; Mismatches 69; Indels 34; Gaps 5;

QY 6 LLILIMVHPSGSCALWVSQPPEIRTLGSSAFPLCSFNASQGRLAIGSVTFRDEVVPGKE 65
DB 23 LFFLVTFPVFSKGMNVTQPPVLASSRGVASFCEYESS-GRADVRVTVLREAGSQVTE 81
QY 66 VRNGTPEFRGLAPLASSRFL--HDHQAEHLHVRDGHDSIYVCRVEVL--GLGVGT 119
DB 82 VCAGTYVDELFDDSTCIGTSRGKNKNTLTIQGLRAMDTGLYCKVELMYPPIYVGI 141
QY 120 GNGTRL-VVEKEHPQLGAGTVLLLRAGFVAVSFLSVAGSTVYVQKGC 166
DB 142 GNGTQIVYIAKEK-----KPSYIRGLC 163

RESULT 5
TVA2 MOUSE
ID TVA2 MOUSE STANDARD; PRT; 132 AA.
AC P01739;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

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DE T-cell receptor alpha chain V region 2B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (CLONE TT11).
RX MEDLINE=85036634; PubMed=6548551;
RA Chien Y., Becker D.M., Lindsten T., Okamura M., Cohen D.I.,
RA Davis M.M.;
RT "A third type of murine T-cell receptor gene.";
RL Nature 312:31-35(1984).
DR HSP; P01738; ITCR.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; T-cell.
FT CHAIN 1 20 T-cell receptor alpha chain V region 2B4.
FT DOMAIN 21 132 V segment.
FT DOMAIN 114 117 D segment.
FT DOMAIN 118 132 J segment.
FT CARBOHYD 42 42 N-linked (GlcNAc...).
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14668 MW; CABBF6CFIDD3448B CRC64;

Query Match 10.4%; Score 106; DB 1; Length 132;
Best Local Similarity 25.8%; Pred. No. 0.12;
Matches 40; Conservative 22; Mismatches 45; Indels 48; Gaps 9;

QY 3 WLLILLIMVHPSGSCALWVS-----QPPEIRTLGSSAFPLCSFNASQGRLAIGSVTW 55
DB 12 WLLL-----NWNVSQNVQSPESLIYVEGARTSLNCTFDSASQY----FWW 55
QY 56 PRDEVVPGKEVR-----NGTPEFRGLAPLASSRFLHDSIYVCRVEVLHVRDGHDSIYVC 108
DB 56 YRQH--SGKAPKALMSIFSNKEK-EGRTIHLNKAHLH--FSLHSDSQPSDSALYLC 109
QY 109 RVEVLGLGVGTGNGTRLVVEKEHPQLGAGTVLLLR 143
DB 110 AVTIYG-----GSGNKLI-----FGTGILLSVK 132

RESULT 6
Q9Z1A7 PRELIMINARY; PRT; 174 AA.
ID Q9Z1A7;
AC Q9Z1A7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CTLA-4.
GN Name=CTLA-4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ACI;
RA Oaks M.K.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U90271; AAD00697.1; -.
DR HSP; P09793; 1DQT.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTLA4.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 1.
DR PRINTS; PR01720; CTLANTIGEN4.

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DR SMART; SMO0409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
SQ SEQUENCE 174 AA; 19327 MW; 8CAA0FE73AA18872 CRC64;

Query Match
  10.2%; Score 104; DB 2; Length 174;
Matches 41; Conservative 23; Mismatches 56; Indels 18; Gaps 7;

Qy 5 LLLILIMVHFGSCALMWSQPPETIRLEGGSAFLPC-----SFNASQGRLAIGSVTWFRDEV 60
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 VLLSLFPIFSEAIQVTPSVVLLASSHGVSAPFCEYASSHNTDEVRTVLQRT--NDQV 81
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 61 VPGKEVNGPPEFRGLA-----FLASSRFLHDAELHIRDVRGHDASIYVCRVEVL--- 113
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 T---EVCATFTVNTLGLDFDFCSGTF-NESRVNLTIGQLRAADTGLYFCKVELMYP 137
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 114 GLGVGTGNGTRL-VVEKE 130
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 138 PYFVGNGGTQIVYIAKE 155
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
Q90XW9
ID Q90XW9 PRELIMINARY; PRT; 164 AA.
AC Q90XW9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE New antigen receptor (Fragment).
OS Orectolobus maculatus (spotted wobbegong).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
OC Orectolobidae; Orectolobus.
OX NCBI_TaxID=168098;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21451048; PubMed=11566324;
RX Nuttall S.D.; Krishnan U.V.; Hattarki M.; De Gori R.; Irving R.A.;
RA Hudson P.J.;
RT "Isolation of the new antigen receptor from wobbegong sharks, and use
  as a scaffold for the display of protein loop libraries.";
RL Mol. Immunol. 38:313-326(2001).
DR GO; GO:0004872; F:receptor activity; IEA.
DR EMBL; AF336091; AAK97359.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0409; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW Receptor.
FT NON TER 164
SQ SEQUENCE 164 AA; 18009 MW; AC12ADCC542AA567 CRC64;

Query Match
  10.0%; Score 102.5; DB 2; Length 164;
Best Local Similarity 27.1%; Pred. No. 0.32;
Matches 42; Conservative 16; Mismatches 54; Indels 43; Gaps 7;

Qy 5 LLLILIMVHFGSCALMWSQPPETIRLE-GSSAFPLCSP-NASQGRLAIGSVTWFRDEVVP 62
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 LLSVLLALFNVFTAWVDQTPRTATKETGESLTINCVLRDASVGSERTG--WYRTKLGS 61
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 63 GKE-----VANGTPEPRGLAPLASSRFLHDAELHIRDVRGHDASIYVCRV 110
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 TNEQTISIGGRYVETVKNKSKS-----SLRINDLEVSIGTKCG- 102
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 111 EVLGLGVGTGNGRLVVEKEHPQLGAGTVLLLRAG 145
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 103 ---GLATLAPYQLISYEK-----GAGTVLTVKPG 130
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8

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Q8TDA6
ID Q8TDA6 PRELIMINARY; PRT; 160 AA.
AC Q8TDA6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CTIA4 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP Guo J.H.; Fan M.W.; Bian Z.; Jia R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46806; AAL96664.1; -.
DR FIR; I84732; I84732.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008096; CTIA4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR PRINTS; PR01720; CTLANTIGEN4.
DR SMART; SMO0406; IG; 1.
FT NON TER 160
SQ SEQUENCE 160 AA; 17470 MW; 1385B4644F63836F CRC64;

Query Match
  9.8%; Score 100; DB 2; Length 160;
Best Local Similarity 27.9%; Pred. No. 0.53;
Matches 39; Conservative 18; Mismatches 63; Indels 20; Gaps 5;

Qy 6 LLLILIMVHFGSC-ALMWSQPPETIRLEGGSAFLPCSFNASQGRLAIGSVTWFRDEVVPGK 64
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 LLLFELLFIPVFCAMHVAQPAVVLASSRGTSFVCEY-ASPGKATEVRVTVLRQADSQVT 82
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 65 EVRNGTPEFRGLAPLASSRFLHD-----HQELHIRDVRGHDASIYVCRVEVL-- 113
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 83 EVCAATYMGNELT-----FLDDSICTGTSSGNQVNLTIQGLRAMDTGLYCKVELMYP 136
   :|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 114 -GLGVGTGNGTRLVVEKEHP 132
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 137 PPYLGLGNGTQIYVIDPEP 156
   |||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
Q6LBN1
ID Q6LBN1 PRELIMINARY; PRT; 152 AA.
AC Q6LBN1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE V beta 5.5 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Thymus;
RC George Jr J.P.; Schroeder Jr H.W.;
RL Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
DR EMBL; X56142; CAA39607.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SMO0409; IG; 1.
DR SMART; SMO0408; IGC2; 1.
DR SMART; SMO0406; IG; 1.
DR PROSITE; PS0835; IG_LIKE; 1.

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FT  NON TER      1
SQ  SEQUENCE      152 AA; 16242 MW;  D9C6F0EE8ED8DE2  CRC64;

Query Match      9.7%; Score 98.5; DB 2; Length 152;
Best Local Similarity 25.0%; Pred. No. 0.68;
Matches 33; Conservative 25; Mismatches 51; Indels 23; Gaps 6;

QY  1  MAWMLLLILIMVHPGSCALWVSQPE--IRTLGSSAFPCSPFNASQGLAIGSVTWPRD 58
    27  LCWVLCLLDL---GAGSVETGVTQSPHILKIT-RGQVTLRCSSQSGH-----NTVSWYQQ 77
    59  EVVPG-----KEVRNGTPEFFGRGLAPLASSRFLHCHOAELHIRDVRGHDASIYVCRV 110
    78  ALGQGPQPIFOFYREEENG---RGNPPRFGSLQPPNYSELNVNALELDDSDALYLCLAS 133
    111  EVILGLGVGTGNG 122
    134  SGLAGMGSSSG 145

RESULT 10
CAA39607 PRELIMINARY; PRT; 152 AA.
ID  CAA39607 PRELIMINARY; PRT; 152 AA.
DT  02-MAR-2004 (TREMBLrel. 27, Created)
DT  02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE  V beta 5.5 protein (Fragment).
DE  V BETA 5.5.
GN  Homo sapiens (Human).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
[1] RN
RP  SEQUENCE OF 134-152 FROM N.A.
RC  TISSUE=Thymus;
RA  George Jr J.F., Schroeder Jr H.W.;
RL  Submitted (OCT-1990) to the EMBL/GenBank/DBJ databases.
DR  EMBL; X56142; CAA39607.1; -.
KW  T-cell.
FT  NON TER      1
SQ  SEQUENCE      152 AA; 16242 MW;  D9C6F0EE8ED8DE2  CRC64;

Query Match      9.7%; Score 98.5; DB 2; Length 152;
Best Local Similarity 25.0%; Pred. No. 0.68;
Matches 33; Conservative 25; Mismatches 51; Indels 23; Gaps 6;

QY  1  MAWMLLLILIMVHPGSCALWVSQPE--IRTLGSSAFPCSPFNASQGLAIGSVTWPRD 58
    27  LCWVLCLLDL---GAGSVETGVTQSPHILKIT-RGQVTLRCSSQSGH-----NTVSWYQQ 77
    59  EVVPG-----KEVRNGTPEFFGRGLAPLASSRFLHCHOAELHIRDVRGHDASIYVCRV 110
    78  ALGQGPQPIFOFYREEENG---RGNPPRFGSLQPPNYSELNVNALELDDSDALYLCLAS 133
    111  EVILGLGVGTGNG 122
    134  SGLAGMGSSSG 145

RESULT 11
LV6E HUMAN
ID  LV6E HUMAN STANDARD; PRT; 131 AA.
AC  P06319;
DT  01-JAN-1988 (Rel. 06, Created)
DT  01-JAN-1988 (Rel. 06, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig lambda chain V-VI region EB4 precursor.
DE  V BETA 5.5.
GN  Homo sapiens (Human).
OS  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
[1] RN

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